



# **STIC Search Report**

## **Biotech-Chem Library**

STIC Database Tracking Number: 163003

**TO: Sean McGarry**  
**Art Unit: 1635**  
**Location: rem/2d19/2c18**  
**Serial Number: 09/927046**

**Tuesday, May 17, 2005**

**From: Beverly Shears**  
**Location: Biotech-Chem Library**  
**REM 1A54**  
**Phone: 571-272-2528**  
**beverly.shears@uspto.gov**

### **Search Notes**

**This Page Blank (uspto)**

From: McGarry, Sean  
Sent: Tuesday, May 10, 2005 10:18 AM  
To: STIC-Biotech/ChemLib  
Subject: SEQ SEARCH 09/927046

Sean McGarry  
AU 1635  
REM 02D19 Office  
REM 2C18 Mailbox  
X20761

Please a search of SEQ ID NOS: 143 and 2332 length limited (nt  $\leq$  100).

Thank You

seq 143 - 17NA  
2332 - 38NA

\*\*\*\*\*  
STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

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Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIS: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
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Other(Specify): \_\_\_\_\_

Date completed: \_\_\_\_\_

Searcher: Beverly e 2528

Terminal time: \_\_\_\_\_

Elapsed time: \_\_\_\_\_

CPU time: \_\_\_\_\_

Total time: \_\_\_\_\_

Number of Searches: \_\_\_\_\_

Number of Databases: \_\_\_\_\_

Search Site

\_\_\_\_\_ STIC  
\_\_\_\_\_ CM-1  
\_\_\_\_\_ Pre-S

Type of Search

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\_\_\_\_\_ A.A. Sequence  
\_\_\_\_\_ Structure  
\_\_\_\_\_ Bibliographic

Vendors

\_\_\_\_\_ JG  
\_\_\_\_\_ STN  
\_\_\_\_\_ Dialog  
\_\_\_\_\_ APS  
\_\_\_\_\_ Geninfo  
\_\_\_\_\_ SDC  
\_\_\_\_\_ DARC/Questel  
\_\_\_\_\_ Other CGN

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09/927046

FILE 'REGISTRY' ENTERED AT 16:17:32 ON 16 MAY 2005

L1 121 S CCUGAUUUCUUGCAGG | CCUGCAAUCUGAUGAGGCCGUUAGGCCGAAAAUCAGG/SQSN  
L2 4 S L1 AND SQL=<100

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CN GenBank AX580494 (9CI) (CA INDEX NAME)  
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SQL 38

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CN GenBank AX578305 (9CI) (CA INDEX NAME)  
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SQL 17

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L2 ANSWER 3 OF 4 REGISTRY COPYRIGHT 2005 ACS on STN  
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OTHER NAMES:

CN 332: PN: WO0211674 SEQID: 2332 claimed RNA

CI MAN

SQL 38

SEQ 1 ccugcaaucu gaugaggccg uuaggccgaa aaaucagg  
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HITS AT: 1-38

REFERENCE 1: 136:194272

L2 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2005 ACS on STN  
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CN RNA, (C-C-U-G-A-U-U-U-C-A-U-U-G-C-A-G-G) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 144: PN: WO0211674 SEQID: 143 claimed RNA

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HITS AT: 1-17

REFERENCE 1: 136:194272

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L3 1 S L2

L3 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN  
ED Entered STN: 15 Feb 2002  
ACCESSION NUMBER: 2002:122738 CAPLUS

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09/927046

DOCUMENT NUMBER: 136:194272  
 TITLE: Ribozymes and antisense oligonucleotides for the inhibition of gene expression by calcium-activated chloride channel-1 gene CLCA-1  
 INVENTOR(S): Thompson, James; McSwiggen, James; McKenzie, Timothy; Ayers, David; Szymkowski, David E.; Grupe, Andrew  
 PATENT ASSIGNEE(S): Ribozyme Pharmaceuticals, Incorporated, USA; Syntex (U.S.A.) LLC  
 SOURCE: PCT Int. Appl., 152 pp.  
 CODEN: PIXXD2  
 DOCUMENT TYPE: Patent  
 LANGUAGE: English  
 FAMILY ACC. NUM. COUNT: 1  
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002011674	A2	20020214	WO 2001-US24970	20010809
WO 2002011674	A3	20030925		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
US 2003064946	A1	20030403	US 2001-927046	20010809
PRIORITY APPLN. INFO.:			US 2000-224383P	P 20000809

AB Nucleic acid mols., including antisense and enzymic nucleic acid mols., such as hammerhead ribozymes, DNazymes, and GeneBlocs, which modulate the expression of calcium-activated chloride channels (CLCA1, CLCA2, CLCA3, and CLCA4) are provided. A target discovery target validation approach was used for finding genes that are involved in chronic mucous hypersecretion. The reporter system consists of a plasmid construct, termed pMUC5AC-EGFP, bearing a gene coding for green fluorescent protein (GFP). The promoter region of the GFP gene is replaced by a portion of the mucin 5AC promoter sufficient to direct efficient transcription of the GFP gene; the plasmid also contains the neomycin drug resistance gene. The cell line selected as host for these studies, NCI-H292 (ATCC CRL-1848), is derived from a human lung mucoepidermoid carcinoma. A ribozyme library with two randomized regions comprising six-nucleotide binding "arms" is used to enrich cells for non-responders to mucin induction and a bioinformatics approach used to identify human CLCA1 as a regulator of MUC5AC expression. Antisense, hammerhead, DNzyme, NCH, amberzyme, zinzyme, and G-Cleaver ribosome binding/cleavage sites in CLCA1 were identified. The nucleic acid mols. are individually analyzed by computer folding to assess whether the sequences fold into the appropriate secondary structure and to anneal to various sites in the RNA target. Those nucleic acid mols. with unfavorable intramol. interactions such as between the binding arms and the catalytic core are eliminated from consideration. Varying binding arm lengths can be chosen to optimize activity.

IT 398240-93-2

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09/927046

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
(Biological study)  
(CLCA-1 gene target region for hammerhead ribozyme; ribozymes and  
antisense oligonucleotides for the inhibition of gene expression by  
calcium-activated chloride channel-1 gene CLCA-1)

IT 399091-50-0

RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study);  
USES (Uses)  
(hammerhead ribozyme; ribozymes and antisense oligonucleotides for  
the inhibition of gene expression by calcium-activated chloride  
channel-1 gene CLCA-1)

(FILE 'MEDLINE, BIOSIS, EMBASE' ENTERED AT 16:21:55 ON 16 MAY 2005)

L4 0 S L2

FILE 'HOME' ENTERED AT 16:22:05 ON 16 MAY 2005

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09/927046

=> d his

(FILE 'HOME' ENTERED AT 16:08:34 ON 16 MAY 2005)  
DEL HIS Y

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FILE 'CAPLUS' ENTERED AT 16:20:22 ON 16 MAY 2005

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FILE 'CAPLUS' ENTERED AT 16:21:17 ON 16 MAY 2005  
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L4 0 S L2

FILE 'HOME' ENTERED AT 16:22:05 ON 16 MAY 2005

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MC Garry, S.  
09/19/27046 Page 1  
Seq. ID 143 & 2332

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2005, 16:49:04 ; Search time 488.055 Seconds  
(without alignments)  
1687.800 Million cell updates/sec

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Perfect score: 17  
Sequence: 1 ccgaaunacagcag 17

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 2238514

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

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2: gb\_hg:\*  
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8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sra:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	17	100.0	17	6	AX578305 Sequence
2	16	94.1	17	6	AX578304 Sequence
3	16	94.1	17	6	AX578867 Sequence
4	15	88.2	15	6	AX583575 Sequence
5	15	88.2	15	6	AX583576 Sequence
6	15	88.2	15	6	AX583577 Sequence
7	15	88.2	17	6	AX578303 Sequence
8	15	88.2	17	6	AX578304 Sequence
9	14	82.4	15	6	AX583574 Sequence
10	14	82.4	17	6	AX578306 Sequence
11	14	82.4	19	6	AX699218 Sequence
12	13.4	78.8	22	6	AX771264 Sequence
13	13.4	78.8	52	6	AX956812 Sequence
14	13	76.5	15	6	AX583578 Sequence
15	13	76.5	17	6	AX579409 Sequence
16	13	76.5	17	6	AX579833 Sequence
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20	12.8	75.3	80	6	CO116609 Sequence
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## ALIGNMENTS

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LOCUS Sequence 143 from Patent WO0211674.  
AX578305  
ACCESSION AX578305.1 GI:27647507  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Thompson, J., McSwigen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.  
TITLE Method and reagent for the inhibition of calcium activated chloride  
JOURNAL channel-1 (c1ca-1)  
Patent: WO 0211674-A 143 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;  
Thompson, James (US)

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QY 1 CCUAAUUCUAUUGCAGG 17  
DB 1 CCTGATTCATTCAGG 17

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LOCUS Sequence 142 from Patent WO0211674.  
AX578304  
ACCESSION AX578304  
VERSION AX578304.1 GI:27647506  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Thompson, J., McSwigen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.  
TITLE Method and reagent for the inhibition of calcium activated chloride  
JOURNAL channel-1 (c1ca-1)  
Patent: WO 0211674-A 142 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;  
Thompson, James (US)

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LOCUS Sequence 705 from Patent WO0211674.  
AX578867  
ACCESSION AX578867  
VERSION AX578867.1 GI:27648069  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Thompson, J., McSwigen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.  
TITLE Method and reagent for the inhibition of calcium activated chloride  
JOURNAL channel-1 (c1ca-1)  
Patent: WO 0211674-A 705 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;  
Thompson, James (US)

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AX583575  
ACCESSION AX583575  
VERSION AX583575.1 GI:27655385  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE  
AUTHORS Thompson, J., McSwigen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.  
TITLE Method and reagent for the inhibition of calcium activated chloride  
JOURNAL channel-1 (c1ca-1)  
Patent: WO 0211674-A 5413 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;  
Thompson, James (US)

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Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION AX583576  
VERSION AX583576.1 GI:27655386  
KEYWORDS  
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ORGANISM  
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other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Thompson,J., Mcswigen,J., McKenzie,T., Ayers,D., Szymkowski,D.E. and Grube,A.  
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)  
JOURNAL Patent: WO 0211674-A 5414 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)  
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RESULT 6  
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LOCUS Sequence 5415 from Patent WO0211674.  
ACCESSION AX583577  
VERSION AX583577.1 GI:27655387  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Thompson,J., Mcswigen,J., McKenzie,T., Ayers,D., Szymkowski,D.E. and Grube,A.  
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)  
JOURNAL Patent: WO 0211674-A 5415 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)  
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Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TGATTCATTCGAG 15  
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RESULT 7  
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VERSION AX578303.1 GI:27647505  
KEYWORDS  
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ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1  
AUTHORS Thompson,J., Mcswigen,J., McKenzie,T., Ayers,D., Szymkowski,D.E. and Grube,A.  
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)  
JOURNAL Patent: WO 0211674-A 141 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)  
FEATURES  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 88.2%; Score 15; DB 6; Length 17;  
Best Local Similarity 60.0%; Pred. No. 3.5e+03;  
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAGCA 15  
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Db 3 CCTGATTCATTCGCA 17

RESULT 8  
CQ306794 88 bp DNA linear PAT 23-JAN-2004  
LOCUS Sequence 17899 from Patent WO0186003.  
ACCESSION CQ306794  
VERSION CQ306794.1 GI:41267371  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1  
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human lung  
JOURNAL Patent: WO 0186003-A 17899 15-NOV-2001;  
Aeonica, Inc. (US)  
FEATURES  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
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ORIGIN  
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Best Local Similarity 60.0%; Pred. No. 3.2e+03;  
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAGCA 15  
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Db 63 CCTGATTCATTGCA 77

RESULT 9  
AX583574LOCUS AX583574 15 bp DNA linear PAT 10-JAN-2003  
DEFINITION Sequence 5412 from Patent WO211674.  
ACCESSION AX583574  
VERSION AX583574.1 GI:27655384  
KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE

AUTHORS

TITLE

JOURNAL Thompson, J., McSwiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.  
Method and reagent for the inhibition of calcium activated chloride  
channel-1 (Clca-1)  
Patent: WO 0211674-A 5412 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;  
Thompson, James (US)  
Location/Qualifiers

FEATURES

source

1. 15

/organism="synthetic construct"

/mol\_type="unassigned DNA"

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/note="Enzymatic Nucleic Acid"

ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 15;  
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAGUC 14  
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Db 2 CCTGATTCATTGC 15

RESULT 10

LOCUS AX578306 17 bp RNA linear PAT 10-JAN-2003

DEFINITION Sequence 144 from Patent WO0211674.  
ACCESSION AX578306  
VERSION AX578306.1 GI:27647508  
KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1  
Thompson, J., McSwiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.  
and Grube, A.  
Method and reagent for the inhibition of calcium activated chloride  
channel-1 (Clca-1)  
Patent: WO 0211674-A 144 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;  
Thompson, James (US)  
Location/Qualifiers

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. 17

/organism="Homo sapiens"

/mol\_type="unassigned RNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 17;  
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Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAUUCUUCAGAG 17  
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Db 1 GATTCATTGCAG 14RESULT 11  
AX699218/cLOCUS AX699218 19 bp DNA linear PAT 29-MAY-2003  
DEFINITION Sequence 159 from Patent WO03000727.  
ACCESSION AX699218  
VERSION AX699218.1 GI:29499868  
KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE

AUTHORS

TITLE

JOURNAL

Zhang, Y., Moffatt, M., Cookson, W. and Tinsley, J.O.  
Atopy  
Patent: WO 03000727-A 159 03-JAN-2003;  
ISIS INNOVATION LIMITED (GB)  
Location/Qualifiers

FEATURES

source

1. 19

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/note="Primer"

ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 19;  
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Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAUUCUUCAGAG 17  
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Db 19 GATTCATTGCAG 6

RESULT 12

LOCUS AX771264 22 bp DNA linear PAT 02-JUL-2003  
DEFINITION Sequence 12 from Patent WO03038079.  
ACCESSION AX771264  
VERSION AX771264.1 GI:32438307  
KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE

AUTHORS

TITLE

JOURNAL Aerts, J.M. and Boot, R.G.  
A mammalian mucinase, its recombinant production, and its use in  
therapy or prophylaxis against diseases in which mucus is involved  
or infectious diseases  
Patent: WO 03038079-A 12 08-MAY-2003;  
Macrozyme B.V. (NL)  
Location/Qualifiers

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. 22

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/mol\_type="unassigned DNA"

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/note="Primer HAS3-A-tail"

ORIGIN

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Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 CUGAUUUCAGAG 16  
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Db 8 CTGATTTATTGCAG 22

RESULT 13

LOCUS AX956812/c

DEFINITION Sequence 17 from Patent EP1367120.  
ACCESSION AX956812  
VERSION AX956812.1 GI:40785287  
KEYWORDS

SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE  
AUTHORS 1 Takeshima, S., Sogabe, A. and Oka, M.  
TITLE Modified pyrroloquinoline quinone (PQQ) dependent glucose dehydrogenase with superior substrate specificity and stability  
JOURNAL Patent: EP 1367120-A 17 03-DEC-2003;  
TOYO BOSEKI KAKUSHIKI KAISHA (JP)  
FEATURES  
source 1.52  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
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Best Local Similarity 53.3%; Pred. No. 2.7e+04;  
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
Qy 3 UGAUUCAUUGCAGG 17  
Db 15 TGATTGATTGCAGG 1  
RESULT 14  
AX583578 15 bp DNA linear PAT 10-JAN-2003  
LOCUS  
DEFINITION Sequence 5416 from Patent WO0211674.  
ACCESSION AX583578  
VERSION AX583578.1 GI:27655388  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE  
AUTHORS 1 Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E. and Grube, A.  
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)  
JOURNAL Patent: WO 0211674-A 5416 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)  
FEATURES  
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Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 AUUCAUUGCAGG 17  
Db 1 ATTTCATTCGAGG 13  
RESULT 15  
AX579409 17 bp RNA linear PAT 10-JAN-2003  
LOCUS  
DEFINITION Sequence 1247 from Patent WO0211674.  
ACCESSION AX579409  
VERSION AX579409.1 GI:27648611  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1 Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E. and Grube, A.  
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)  
JOURNAL Patent: WO 0211674-A 1247 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)  
FEATURES  
source 1.17  
/organism="Homo sapiens"  
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ORIGIN  
Query Match 76.5%; Score 13; DB 6; Length 17;  
Best Local Similarity 61.5%; Pred. No. 4.7e+04;  
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 AUUCAUUGCAGG 17  
Db 1 ATTTCATTCGAGG 13  
RESULT 16  
AX579833 17 bp RNA linear PAT 10-JAN-2003  
LOCUS  
DEFINITION Sequence 1671 from Patent WO0211674.  
ACCESSION AX579833  
VERSION AX579833.1 GI:27649035  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS 1 Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E. and Grube, A.  
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)  
JOURNAL Patent: WO 0211674-A 1671 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)  
FEATURES  
source 1.17  
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/mol\_type="unassigned RNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 76.5%; Score 13; DB 6; Length 17;  
Best Local Similarity 53.8%; Pred. No. 4.7e+04;  
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCUGAUUUCAGG 13  
Db 5 CCTGATTTCATTG 17  
RESULT 17  
CQ549043 60 bp DNA linear PAT 30-JAN-2004  
LOCUS  
DEFINITION Sequence 18678 from Patent WO0210449.  
ACCESSION CQ549043  
VERSION CQ549043.1 GI:41515470  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Paigler, S.  
Oligonucleotide library for detecting rna transcripts and splice

variants that populate a transcriptome  
Patent: WO 0210449-A 18678 07-FEB-2002;  
Compugen Inc. (US)  
Location/Qualifiers  
1. .60  
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/mol\_type="unassigned DNA"  
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ORIGIN

Query Match 76.5%; Score 13; DB 6; Length 60;  
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OY 4 GAUUUCAUUGCAG 16  
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30 GATTTCATTGCAG 42

Db

RESULT 18  
AX496844/c 67 bp DNA linear PAT 26-SEP-2002  
LOCUS  
DEFINITION Sequence 18 from Patent WO02059371.  
ACCESSION AX496844  
VERSION AX496844.1 GI:23342364  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.

REFERENCE  
AUTHORS  
1 Myrick,J., Ren,B., Robert,F., Simon,I. and Young,R.A.  
TITLE Genome-wide location and function of dna binding proteins  
JOURNAL Patent: WO 02059371-A 18 01-AUG-2002;  
WHITEHEAD BIOMEDICAL INST (US)  
Location/Qualifiers  
1. .67  
/organism="synthetic construct"  
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ORIGIN

Query Match 76.5%; Score 13; DB 6; Length 67;  
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Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 3 UGAUUUCAUUGCA 15  
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43 TGATTTCATTGCA 31

Db

RESULT 19  
CQ081942/c 80 bp DNA linear PAT 20-JAN-2004  
LOCUS  
DEFINITION Sequence 17742 from Patent WO0157278.  
ACCESSION CQ081942  
VERSION CQ081942.1 GI:41051811  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
1 Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
JOURNAL analysis of gene expression in human hela cells or other human  
Patent: WO 0157278-A 17742 09-AUG-2001;  
Aeomica, Inc. (US)  
Location/Qualifiers  
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FEATURES  
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/db\_xref="taxon:9606"  
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AB002059.1, EVALUE 6.00e-38"

ORIGIN

Query Match 75.3%; Score 12.8; DB 6; Length 80;  
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Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 CUGAUUUCAGCAG 17  
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57 CTGATTGCATTTCAGG 42

Db

RESULT 20  
CQ116609/c 80 bp DNA linear PAT 21-JAN-2004  
LOCUS  
DEFINITION Sequence 25468 from Patent WO0157272.  
ACCESSION CQ116609  
VERSION CQ116609.1 GI:41086479  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
1 Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
JOURNAL analysis of gene expression in human placenta  
Patent: WO 0157272-A 25468 09-AUG-2001;  
Aeomica, Inc. (US)  
Location/Qualifiers  
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6.7-EST HUMAN HIT: BF311025.1, EVALUE 1.00e-37-NT HIT:  
AB002059.1, EVALUE 6.00e-38"

ORIGIN

Query Match 75.3%; Score 12.8; DB 6; Length 80;  
Best Local Similarity 56.2%; Pred. No. 5.7e+04;  
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 CUGAUUUCAGCAG 17  
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57 CTGATTGCATTTCAGG 42

Db

RESULT 21  
CQ155325/c 80 bp DNA linear PAT 21-JAN-2004  
LOCUS  
DEFINITION Sequence 25347 from Patent WO0157276.  
ACCESSION CQ155325  
VERSION CQ155325.1 GI:41162677  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
1 Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
JOURNAL analysis of gene expression in human bone marrow  
Patent: WO 0157276-A 25347 09-AUG-2001;  
Aeomica, Inc. (US)  
Location/Qualifiers  
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FEATURES  
source



FEATURES  
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ORIGIN  
Query Match 75.3%; Score 12.8; DB 6; Length 80;  
Best Local Similarity 56.2%; Pred. No. 5.7e+04;  
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 CUGAUUUCAUUGCAGG 17  
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57 CTGATTGATTCAGG 42

RESULT 26  
LOCUS CQ350689 80 bp DNA linear PAT 23-JAN-2004  
DEFINITION Sequence 24783 from Patent WO0157275.  
ACCESSION CQ350689  
VERSION CQ350689.1 GI:41299760  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human brain  
JOURNAL Patent: WO 0157275-A 24783 09-AUG-2001;  
Acemica, Inc. (US)  
FEATURES  
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1. .80  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AC002472.3-EXPRESSED IN BRAIN, SIGNAL = 13-BEST\_HUMAN HIT: BF311025.1, EVALU0 1.00e-37-NT HIT: AB002059.1, EVALU0 6.00e-38"

ORIGIN  
Query Match 75.3%; Score 12.8; DB 6; Length 80;  
Best Local Similarity 56.2%; Pred. No. 5.7e+04;  
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 CUGAUUUCAUUGCAGG 17  
|||:|||||  
57 CTGATTGATTCAGG 42

RESULT 27  
LOCUS CR378747 86 bp DNA linear STS 24-MAR-2004  
DEFINITION Arabidopsis thaliana transposon insertion STS GT\_3.7348, sequence tagged site.  
ACCESSION CR378747  
VERSION CR378747.1 GI:45725203  
KEYWORDS STS; STS, sequence tagged site.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
AUTHORS Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B., Walsh, S., Langham, S., Legrys, C., Jones, J.D.G. and Bevan, M.  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 86)

AUTHORS Clarke, J.H.  
TITLE Direct Submission  
JOURNAL Submitted (22-MAR-2004) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK  
COMMENT AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a gene trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. \_3 denotes a sequence derived from the 3' end of the transposon, \_5 denotes a sequence derived from the 5' end of the transposon BBSRC GARNER, ATIS project  
On-line seed stock requests: [http://nasc.nott.ac.uk/NASC\\_stock\\_code/](http://nasc.nott.ac.uk/NASC_stock_code/) N174684.

FEATURES  
source  
Location/Qualifiers  
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/organism="Arabidopsis thaliana"  
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/clone="AP001305"  
1. .86  
/standard\_name="GT\_3.7348"

ORIGIN  
Query Match 75.3%; Score 12.8; DB 11; Length 86;  
Best Local Similarity 56.2%; Pred. No. 5.7e+04;  
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 CUGAUUUCAUUGCAGG 16  
|||:|||||  
73 CCGATTTCATTCAGG 58

RESULT 28  
LOCUS CQ001210 100 bp DNA linear PAT 16-JAN-2004  
DEFINITION Sequence 12672 from Patent EP1260592.  
ACCESSION CQ001210  
VERSION CQ001210.1 GI:41007848  
KEYWORDS  
SOURCE Escherichia coli  
ORGANISM Escherichia coli  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

REFERENCE  
1 Donner, H., Drescher, B., Huber, A. and Weber, J.  
AUTHORS Biochip  
TITLE Patent: EP 1260592-A 12672 27-NOV-2002;  
JOURNAL MWG -Biotech AG (DE)  
FEATURES  
source  
Location/Qualifiers  
1. .100  
/organism="Escherichia coli"  
/mol\_type="unassigned DNA"  
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/note="Y141 B4279 U00096 complement(449671\_\_450999)"

ORIGIN  
Query Match 75.3%; Score 12.8; DB 6; Length 100;  
Best Local Similarity 62.5%; Pred. No. 5.7e+04;  
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 CUGAUUUCAUUGCAGG 17  
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11 CTGATGACATTCAGG 26

RESULT 29  
LOCUS AX998611 100 bp DNA linear PAT 16-JAN-2004  
DEFINITION Sequence 10074 from Patent EP1260592.  
ACCESSION AX998611  
VERSION AX998611.1 GI:41004957



misc\_feature 1..30  
/note="probe-binding region in DNA of cutaneous supergroup  
B HPV"

ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 30;  
Best Local Similarity 57.1%; Pred. No. 1e+05;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCUGAUUUCAUUGC 14  
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Db 14 CCTGAGTTCATTGC 1

RESULT 34  
CQ794148/c 30 bp DNA linear PAT 19-APR-2004  
LOCUS Sequence 68 from Patent EP1403384.  
DEFINITION CQ794148  
ACCESSION CQ794148  
VERSION CQ794148.1 GI:46406790  
KEYWORDS  
SOURCE Human papillomavirus  
ORGANISM Human papillomavirus  
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;  
Papillomavirus.

REFERENCE 1  
AUTHORS Meijer, C.J. and Snijders, P.J.  
TITLE Method for detecting and typing of cutaneous HPV and primers and probes for use therein  
JOURNAL Patent: EP 1403384-A 68 31-MAR-2004;  
Stichting Researchfonds Pathologie (NL)  
LOCATION/Qualifiers

FEATURES  
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/note="probe-binding region in DNA of cutaneous supergroup  
B HPV"

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Query Match 72.9%; Score 12.4; DB 6; Length 30;  
Best Local Similarity 57.1%; Pred. No. 1e+05;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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Db 14 CCTGAGTTCATTGC 1

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LOCUS Sequence 64 from Patent WO2004029302.  
DEFINITION CQ800113  
ACCESSION CQ800113  
VERSION CQ800113.1 GI:46849034  
KEYWORDS  
SOURCE Human papillomavirus  
ORGANISM Human papillomavirus  
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;  
Papillomavirus.

REFERENCE 1  
AUTHORS Meijer, C.J. and Snijders, P.J.  
TITLE Method for detecting and typing of cutaneous HPV and primers and probes for use therein  
JOURNAL Patent: WO 2004029302-A 64 08-APR-2004;  
Stichting Researchfonds Pathologie (NL)  
LOCATION/Qualifiers

FEATURES  
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B HPV"

ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 30;  
Best Local Similarity 57.1%; Pred. No. 1e+05;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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RESULT 36  
CQ800117/c 30 bp DNA linear PAT 29-APR-2004  
LOCUS Sequence 68 from Patent WO2004029302.  
DEFINITION CQ800117  
ACCESSION CQ800117  
VERSION CQ800117.1 GI:46849038  
KEYWORDS  
SOURCE Human papillomavirus  
ORGANISM Human papillomavirus  
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;  
Papillomavirus.

REFERENCE 1  
AUTHORS Meijer, C.J. and Snijders, P.J.  
TITLE Method for detecting and typing of cutaneous HPV and primers and probes for use therein  
JOURNAL Patent: WO 2004029302-A 68 08-APR-2004;  
Stichting Researchfonds Pathologie (NL)  
LOCATION/Qualifiers

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B HPV"

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Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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RESULT 37  
AR171877 49 bp DNA linear PAT 17-DEC-2001  
LOCUS AR171877/c  
DEFINITION Sequence 10 from patent US 6297365.  
ACCESSION AR171877  
VERSION AR171877.1 GI:17910827  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;  
Papillomavirus.

REFERENCE 1 (bases 1 to 49)  
AUTHORS Adams, C.C., Brenthano, S.T. and Schroth, G.P.  
TITLE Decoy probes  
JOURNAL Patent: US 6297365-A 10 02-OCT-2001;  
Stichting Researchfonds Pathologie (NL)  
LOCATION/Qualifiers

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DB 25 TGATTTCAGTGCAG 12

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DEFINITION Sequence 11 from patent US 6297365.  
ACCESSION AR171878  
VERSION AR171878.1 GI:171910828  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 49)  
AUTHORS Adams,C.C., Brentano,S.T. and Schroth,G.P.  
TITLE Decoy probes  
JOURNAL Patent: US 6297365-A 11 02-OCT-2001;  
FEATURES Location/Qualifiers  
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Query Match 72.9%; Score 12.4; DB 6; Length 49;  
Best Local Similarity 57.1%; Pred. No. 9.8e+04;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGAUUDUCAUUGCAG 16  
:|||||:|||||  
DB 25 TGATTTCAGTGCAG 12

RESULT 39  
LOCUS BD222951 49 bp DNA 11near PAT 17-JUL-2003  
DEFINITION Reversible inhibitory probe.  
ACCESSION BD222951  
VERSION BD222951.1 GI:33032721  
KEYWORDS JP 2002521070-A/10.  
SOURCE JP 2002521070-A/10.  
ORGANISM  
REFERENCE 1 (bases 1 to 49)  
AUTHORS Adams,C.C., Brentano,S.T. and Schroth,G.P.  
TITLE Reversible inhibitory probe  
JOURNAL Patent: JP 2002521070-A 10 16-JUL-2002;  
COMMENT GEN PROBE INC  
OS Synthetic construct  
PN JP 2002521070-A/10  
PD 16-JUL-2002  
PR 30-JUL-1999 JP 2000562561  
PI 31-JUL-1998 US 60/094979  
PI CHRISTOPHER C ADAMS,STEVEN T BRENTANO,GARY P SCHROTH PC  
C12N15/09,C12Q1/68,G01N33/50,C12N15/00  
CC Reversible inhibitory probe  
FH Key Location/Qualifiers  
FT source 1..49  
Location/Qualifiers  
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Query Match 72.9%; Score 12.4; DB 6; Length 49;  
Best Local Similarity 57.1%; Pred. No. 9.8e+04;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGAUUDUCAUUGCAG 16  
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JOB time : 497.055 secs

DB 25 TGATTTCAGTGCAG 12

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DEFINITION Reversible inhibitory probe.  
ACCESSION BD222952  
VERSION BD222952.1 GI:33032722  
KEYWORDS JP 2002521070-A/11.  
SOURCE JP 2002521070-A/11.  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 49)  
AUTHORS Adams,C.C., Brentano,S.T. and Schroth,G.P.  
TITLE Reversible inhibitory probe  
JOURNAL Patent: JP 2002521070-A 11 16-JUL-2002;  
COMMENT GEN PROBE INC  
OS Synthetic construct  
PN JP 2002521070-A/11  
PD 16-JUL-2002  
PR 30-JUL-1999 JP 2000562561  
PI 31-JUL-1998 US 60/094979  
PI CHRISTOPHER C ADAMS,STEVEN T BRENTANO,GARY P SCHROTH PC  
C12N15/09,C12Q1/68,G01N33/50,C12N15/00  
CC Reversible inhibitory probe  
FH Key Location/Qualifiers  
FT source 1..49  
Location/Qualifiers  
1..49  
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ORIGIN  
Query Match 72.9%; Score 12.4; DB 6; Length 49;  
Best Local Similarity 57.1%; Pred. No. 9.8e+04;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGAUUDUCAUUGCAG 16  
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DB 25 TGATTTCAGTGCAG 12

Search completed: May 13, 2005, 18:17:10  
JOB time : 497.055 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
816.004 Million cell updates/sec

Title: US-09-927-046-143

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Sequence: 1 ccugaaucauucagcag 17

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Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	17	6	ABK55772 Human CLC
2	16	94.1	17	6	ABK56334 Human CLC
3	16	94.1	17	6	ABK55771 Human CLC
4	15	88.2	15	6	ABK61042 Human CLC
5	15	88.2	15	6	ABK61044 Human CLC
6	15	88.2	15	6	ABK61043 Human CLC
7	15	88.2	15	6	ABK55770 Human CLC
8	15	88.2	17	6	ABK55770 Human CLC
9	14	82.4	15	6	ABK61041 Human CLC
10	14	82.4	17	6	ABK55773 Human CLC
11	14	82.4	19	10	ADG70258 Human CLC
12	13.4	78.8	22	9	ACC70300 Human CLC
13	13.4	78.8	52	12	ADG16067 Human CLC
14	13.4	78.8	66	2	AAT20442 Human CLC
15	13	76.5	15	6	ABK61045 Human CLC
16	13	76.5	17	6	ABK56876 Human CLC
17	13	76.5	17	6	ABK57300 Human CLC
18	13	76.5	43	12	ADP97171 Human CLC
19	13	76.5	60	6	ABN45930 Human CLC
20	12.8	75.3	20	2	AAV51603 Human CLC

21	12.8	75.3	23	2	AAV51602 Human CLC
22	12.8	75.3	25	9	ACK08857 Human CLC
23	12.8	75.3	32	6	ABK33718 Human CLC
24	12.8	75.3	41	2	AAV50992 Human CLC
25	12.8	75.3	41	2	AAV50971 Human CLC
26	12.8	75.3	41	2	AAV50981 Human CLC
27	12.8	75.3	41	2	AAV50994 Human CLC
28	12.8	75.3	41	2	AAV50994 Human CLC
29	12.8	75.3	41	2	AAV47798 Human CLC
30	12.8	75.3	41	2	AAV47788 Human CLC
31	12.8	75.3	63	2	AAH66424 Human CLC
32	12.8	75.3	80	4	AAI27809 Human CLC
33	12.8	75.3	80	4	AAI27809 Human CLC
34	12.8	75.3	80	4	AAI56782 Human CLC
35	12.8	75.3	80	4	ABA40677 Human CLC
36	12.8	75.3	80	4	AAK50790 Human CLC
37	12.8	75.3	80	4	AAK24792 Human CLC
38	12.8	75.3	80	4	ABK50382 Human CLC
39	12.8	75.3	80	6	ABK54274 Human CLC
40	12.8	75.3	100	8	ACD81396 Human CLC
41	12.8	75.3	100	8	ACD81396 Human CLC
42	12.4	72.9	19	11	ADL70081 Human CLC
43	12.4	72.9	19	11	ADL70081 Human CLC
44	12.4	72.9	20	3	AAZ75567 Human CLC
45	12.4	72.9	25	8	AAI52075 Human CLC
46	12.4	72.9	25	13	ADH45223 Human CLC
47	12.4	72.9	27	13	ADR37819 Human CLC
48	12.4	72.9	41	2	AAV47787 Human CLC
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51	12.4	72.9	41	2	AAV47785 Human CLC
52	12.4	72.9	41	2	AAV47795 Human CLC
53	12.4	72.9	47	3	AAZ69384 Human CLC
54	12.4	72.9	49	3	AAZ58532 Human CLC
55	12.4	72.9	49	3	AAZ58531 Human CLC
56	12.4	72.9	60	6	ABK35208 Human CLC
57	12.4	72.9	60	6	ABK42451 Human CLC
58	12.4	72.9	60	6	ABK46050 Human CLC
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61	12.2	71.8	20	2	AAQ37064 Human CLC
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67	12.2	71.8	23	10	ADC42403 Human CLC
68	12.2	71.8	23	10	ADH94249 Human CLC
69	12.2	71.8	24	6	ABK15883 Human CLC
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71	12.2	71.8	25	2	AAZ78100 Human CLC
72	12.2	71.8	26	3	AAZ91969 Human CLC
73	12.2	71.8	26	3	ABK559052 Human CLC
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96	12.2	71.8	100	8	ACD75158	E. coli K
97	12.2	71.8	100	8	ACD74181	E. coli K
98	12.2	71.8	100	8	ACD75159	E. coli K
99	12.2	71.8	100	8	ACD79939	E. coli K
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ALIGNMENTS

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ID ABK5772 standard; RNA; 17 BP.  
AC ABK5772;  
XX  
XX  
DT 02-JUL-2002 (first entry)  
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XX  
DE Human CLCA1 gene enzymatic nucleic acid #143.  
XX  
XX  
KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
KW acetylcysteine.  
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XX  
OS Homo sapiens.  
XX  
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PN WO20021674-A2.  
XX  
XX  
PD 14-FEB-2002.  
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PF 09-AUG-2001; 2001WO-US024970.  
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PR 09-AUG-2000; 2000US-0224383P.  
XX  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
XX  
PA (SYNT) SYNTX USA LLC.  
XX  
XX  
PA (THOM/) THOMPSON J.  
XX  
XX  
PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;  
PI Grube A;  
XX  
XX  
DR WPI; 2002-217145/27.  
XX  
XX  
PT Enzymatic polynucleotide that down regulates expression of chloride  
PT channel calcium activated gene, useful for treating Chronic obstructive  
PT pulmonary disease (COPD), chronic bronchitis and asthma.  
XX  
XX  
PS Claim 4; Page 55; 152pp; English.  
XX  
XX  
CC The invention relates to enzymatic nucleic acid molecules that down  
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
CC useful as pharmaceutical agents for treating conditions such as chronic  
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
CC that are related to or will respond to the levels of CLCA1 in a cell or  
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
CC hence, are useful for treatment of a patient having a condition  
CC associated with the level of CLCA1, where the invention further comprises  
CC the use of one or more therapies under conditions suitable for the  
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
CC nucleic acids of the invention are also used as diagnostic tools to  
CC examine genetic drift and mutations within diseased cells or to detect  
CC the presence of CLCA1 RNA in a cell. This sequence represents an  
CC enzymatic nucleic acid molecule of the invention  
XX  
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SQ Sequence 17 BP; 3 A; 4 C; 4 G; 0 T; 6 U; 0 Other;

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Best Local Similarity	100.0%;	Pred. No. 63;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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AC ABK56334;  
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XX  
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XX  
KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
KW acetylcysteine.  
XX  
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OS Homo sapiens.  
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PN WO20021674-A2.  
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PD 14-FEB-2002.  
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PF 09-AUG-2001; 2001WO-US024970.  
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PR 09-AUG-2000; 2000US-0224383P.  
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PA (RIBO-) RIBOZYME PHARM INC.  
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PA (SYNT) SYNTX USA LLC.  
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PA (THOM/) THOMPSON J.  
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PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;  
PI Grube A;  
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DR WPI; 2002-217145/27.  
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XX  
PT Enzymatic polynucleotide that down regulates expression of chloride  
PT channel calcium activated gene, useful for treating Chronic obstructive  
PT pulmonary disease (COPD), chronic bronchitis and asthma.  
XX  
XX  
PS Claim 4; Page 67; 152pp; English.  
XX  
XX  
CC The invention relates to enzymatic nucleic acid molecules that down  
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
CC useful as pharmaceutical agents for treating conditions such as chronic  
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
CC that are related to or will respond to the levels of CLCA1 in a cell or  
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
CC hence, are useful for treatment of a patient having a condition  
CC associated with the level of CLCA1, where the invention further comprises  
CC the use of one or more therapies under conditions suitable for the  
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
CC nucleic acids of the invention are also used as diagnostic tools to  
CC examine genetic drift and mutations within diseased cells or to detect  
CC the presence of CLCA1 RNA in a cell. This sequence represents an  
CC enzymatic nucleic acid molecule of the invention  
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XX  
SQ Sequence 17 BP; 4 A; 3 C; 4 G; 0 T; 6 U; 0 Other;

Query Match 94.1%; Score 16; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CUGAUUUCAUUGCAG 16

## RESULT 3

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AC ABK5771;  
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DT 02-JUL-2002 (first entry)  
XX

DE Human CLCA1 gene enzymatic nucleic acid #142.  
XX

KW Human; chloride channel activated 1; CLCA1; ss; antiasthmatic;  
KM antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
KM oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
KW acetylcysteine.

OS Homo sapiens.  
XX

PN WO200211674-A2.  
XX

PD 14-FEB-2002.  
XX

PR 09-AUG-2001; 2001WO-US024970.  
XX

PR 09-AUG-2000; 2000US-0224383P.  
XX

PA (RIBO-) RIBOZYME PHARM INC.  
XX

PA (SYNT) SYNTEX USA LLC.  
XX

PA (THOM/) THOMPSON J.  
XX

PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;  
XX

PI Grupe A;  
XX

PT Enzymatic polynucleotide that down regulates expression of chloride  
channel calcium activated gene, useful for treating Chronic obstructive  
pulmonary disease (COPD), chronic bronchitis and asthma.  
XX

PS Claim 4; Page 55; 152pp; English.  
XX

CC The invention relates to enzymatic nucleic acid molecules that down  
regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
by cleaving RNA derived from the genes. The nucleic acid sequences are  
useful as pharmaceutical agents for treating conditions such as chronic  
obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
fibrosis, obstructive bowel syndrome and any other diseases or conditions  
that are related to or will respond to the levels of CLCA1 in a cell or  
tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
hence, are useful for treatment of a patient having a condition  
associated with the level of CLCA1, where the invention further comprises  
the use of one or more therapies under conditions suitable for the  
treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
nucleic acids of the invention are also used as diagnostic tools to  
examine genetic drift and mutations within diseased cells or to detect  
the presence of CLCA1 RNA in a cell. This sequence represents an  
enzymatic nucleic acid molecule of the invention  
XX

XX Sequence 17 BP; 3 A; 4 C; 3 G; 0 T; 7 U; 0 Other;  
SQ

Query Match 94.1%; Score 16; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAUUGCAG 16  
|||||

DB 2 CCUGAUUUCAUUGCAG 17

## RESULT 4

ABK61042  
ID ABK61042 standard; DNA; 15 BP.

AC ABK61042;  
XX

DT 02-JUL-2002 (first entry)  
XX

DE Human CLCA1 gene enzymatic nucleic acid #5413.  
XX

KW Human; chloride channel activated 1; CLCA1; ss; antiasthmatic;  
KM antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
KM oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
KW acetylcysteine.

OS Homo sapiens.  
XX

PN WO200211674-A2.  
XX

PD 14-FEB-2002.  
XX

PR 09-AUG-2001; 2001WO-US024970.  
XX

PR 09-AUG-2000; 2000US-0224383P.  
XX

PA (RIBO-) RIBOZYME PHARM INC.  
XX

PA (SYNT) SYNTEX USA LLC.  
XX

PA (THOM/) THOMPSON J.  
XX

PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;  
XX

PI Grupe A;  
XX

PT Enzymatic polynucleotide that down regulates expression of chloride  
channel calcium activated gene, useful for treating Chronic obstructive  
pulmonary disease (COPD), chronic bronchitis and asthma.  
XX

PS Claim 4; Page 139; 152pp; English.  
XX

CC The invention relates to enzymatic nucleic acid molecules that down  
regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
by cleaving RNA derived from the genes. The nucleic acid sequences are  
useful as pharmaceutical agents for treating conditions such as chronic  
obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
fibrosis, obstructive bowel syndrome and any other diseases or conditions  
that are related to or will respond to the levels of CLCA1 in a cell,  
tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
hence, are useful for treatment of a patient having a condition  
associated with the level of CLCA1, where the invention further comprises  
the use of one or more therapies under conditions suitable for the  
treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
nucleic acids of the invention are also used as diagnostic tools to  
examine genetic drift and mutations within diseased cells or to detect  
the presence of CLCA1 RNA in a cell. This sequence represents an  
enzymatic nucleic acid molecule of the invention  
XX

XX Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;  
SQ

Query Match 88.2%; Score 15; DB 6; Length 15;  
Best Local Similarity 60.0%; Pred. No. 6.7e+02;

Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAUUGCA 15  
|||:|:|:|:|:|:|  
DB 1 CCTGATTCAATTGCA 15

```

RESULT 5
ABK61044
ID ABRK61044 standard; DNA; 15 BP.
XX
XX ABRK61044;
XX
XX 02-JUL-2002 (first entry)
XX
XX Human CLCA1 gene enzymatic nucleic acid #5415.
DE
XX
XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
XX antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
XX chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
XX oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
XX acetylcysteine.
XX
XX Homo sapiens.
XX
XX MO200211674-A2.
XX
XX 14-FEB-2002.
XX
XX 09-AUG-2001; 2001WO-US024970.
XX
XX 09-AUG-2000; 2000US-0224383P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (SYNT) SYNTAX USA LLC.
XX (THOM/) THOMPSON J.
XX
XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
XX Grube A;
XX
XX WPI; 2002-217145/27.
XX
XX Enzymatic polynucleotide that down regulates expression of chloride
XX channel calcium activated gene, useful for treating Chronic obstructive
XX pulmonary disease (COPD), chronic bronchitis and asthma.
XX
XX Claim 4; Page 139; 152pp; English.
XX
XX The invention relates to enzymatic nucleic acid molecules that down
XX regulate expression of chloride channel calcium activated 1 (CLCA1) genes
XX by cleaving RNA derived from the genes. The nucleic acid sequences are
XX useful as pharmaceutical agents for treating conditions such as chronic
XX obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
XX fibrosis, obstructive bowel syndrome and any other diseases or conditions
XX that are related to or will respond to the levels of CLCA1 in a cell or
XX tissue. The sequences are useful for reducing CLCA1 activity in a cell,
XX hence, are useful for treatment of a patient having a condition
XX associated with the level of CLCA1, where the invention further comprises
XX the use of one or more therapies under conditions suitable for the
XX treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
XX antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
XX nucleic acids of the invention are also used as diagnostic tools to
XX examine genetic drift and mutations within diseased cells or to detect
XX the presence of CLCA1 RNA in a cell. This sequence represents an
XX enzymatic nucleic acid molecule of the invention
XX
XX Sequence 15 BP; 3 A; 2 C; 4 G; 6 T; 0 U; 0 Other;
SQ
Query Match 88.2%; Score 15; DB 6; Length 15;
Best Local Similarity 60.0%; Pred. No. 6.7e+02;
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
OY 3 UGAUUUCAGUUCGAGG 17
Db 1 TGATTTCATTGCAGG 15
RESULT 6
ABK61043
ID ABRK61043 standard; DNA; 15 BP.

```

XX	ABK61043;
AC	
XX	
DT	02-JUL-2002 (first entry)
XX	
DE	Human CLCA1 gene enzymatic nucleic acid #5414.
XX	
KW	Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KM	antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KX	chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW	oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
XX	acetylcysteine.
OS	Homo sapiens.
PN	WO200211674-A2.
XX	
PD	14-FEB-2002.
PF	09-AUG-2001; 2001WO-US024970.
PR	09-AUG-2000; 2000US-0224383P.
PA	(RIBO-) RIBOZYME PHARM INC.
PA	(SYNT) SYNTEX USA LLC.
PA	(THOM) THOMPSON J.
PI	Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
PI	Grupe A;
XX	
DR	WPI: 2002-217145/27.
PT	Enzymatic polynucleotide that down regulates expression of chloride
PT	channel calcium activated gene, useful for treating Chronic obstructive
PT	pulmonary disease (COPD), chronic bronchitis and asthma.
XX	
B6	Claim 4; Page 139; 152pp; English.
XX	
CC	The invention relates to enzymatic nucleic acid molecules that down
CC	regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC	by cleaving RNA derived from the genes. The nucleic acid sequences are
CC	useful as pharmaceutical agents for treating conditions such as chronic
CC	obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC	fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC	that are related to or will respond to the levels of CLCA1 in a cell or
CC	tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC	hence, are useful for treatment of a patient having a condition
CC	associated with the level of CLCA1, where the invention further comprises
CC	the use of one or more therapies under conditions suitable for the
CC	treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC	antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC	nucleic acids of the invention are also used as diagnostic tools to
CC	examine genetic drift and mutations within diseased cells or to detect
CC	the presence of CLCA1 RNA in a cell. This sequence represents an
CC	enzymatic nucleic acid molecule of the invention
SQ	Sequence 15 BP; 3 A; 3 C; 3 G; 6 T; 0 U; 0 Other;
Query Match	88.2%; Score 15; DB 6; Length 15;
Best Local Similarity	60.0%; Pred. No. 6.7e+02;
Matches	9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
OY	2 CUGAUUUCAUUGCAG 16  :: :: :: :: ::  1 CTGATTTCATTGCAG 15
Db	
RESULT 7	
ID	ABKS5770 standard; RNA; 17 BP.
AC	ABKS5770;
XX	

02-JUL-2002 (first entry)  
Human CLCA1 gene enzymatic nucleic acid #141.  
Human; chloride channel, calcium activated 1; CLCA1; 89; antiasthmatic;  
antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
acetylcysteine.  
Homo sapiens.  
WO200211674-A2.  
14-FEB-2002.  
09-AUG-2001; 2001WO-US024970.  
09-AUG-2000; 2000US-0224383P.  
(RIBO-) RIBOZYME PHARM INC.  
(SYNT) SYNTEX USA LLC.  
(THOM/) THOMPSON J.  
Thompson J, Mcswigen J, McKenzie T, Ayers D, Szymkowski DE,  
Grube A,  
WPI; 2002-217145/27.  
Enzymatic polynucleotide that down regulates expression of chloride  
channel calcium activated gene, useful for treating Chronic obstructive  
pulmonary disease (COPD), chronic bronchitis and asthma.  
Claim 4; Page 55; 152pp; English.  
The invention relates to enzymatic nucleic acid molecules that down  
regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
by cleaving RNA derived from the genes. The nucleic acid sequences are  
useful as pharmaceutical agents for treating conditions such as chronic  
obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
fibrosis, obstructive bowel syndrome and any other diseases or conditions  
that are related to or will respond to the levels of CLCA1 in a cell or  
tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
hence, are useful for treatment of a patient having a condition  
associated with the level of CLCA1, where the invention further comprises  
the use of one or more therapies under conditions suitable for the  
treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
nucleic acids of the invention are also used as diagnostic tools to  
examine genetic drift and mutations within diseased cells or to detect  
the presence of CLCA1 RNA in a cell. This sequence represents an  
enzymatic nucleic acid molecule of the invention  
Sequence 17 BP; 3 A; 5 C; 2 G; 0 T; 7 U; 0 Other;  
Query Match 88.2%; Score 15; DB 6; Length 17;  
- Best Local Similarity 100.0%; Pred. No. 6; 8e-02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCUGAUTCAGUCCA 15  
Db 3 CCUGAUTCAGUCCA 17  
RESULT 8  
ABSI7908  
ID ABSI7908 standard; DNA; 88 BP.  
XX ABSI7908;  
AC 19-AUG-2002 (first entry)  
XX Human genome-derived single exon probe ORF from lung SEQ ID No 17899.  
DE

Human; de; single exon probe; asthma; lung cancer; COPD; ILD;  
chronic obstructive pulmonary disease; interstitial lung disease;  
familial idiopathic pulmonary fibrosis; neurofibromatosis;  
tuberculous sclerotic; Gaucher's disease; Niemann-Pick disease;  
Hernandez-Pudlak syndrome; sarcoidosis; pulmonary haemolysis;  
pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;  
pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
primary ciliary dyskinesia; pulmonary hypertension;  
hyaline membrane disease; open reading frame; ORF.  
Homo sapiens.  
WO200186003-A2.  
15-NOV-2001.  
30-JAN-2001; 2001WO-US000665.  
04-FEB-2000; 2000US-0180312P.  
26-MAY-2000; 2000US-0207456P.  
30-JUN-2000; 2000US-00608408.  
03-AUG-2000; 2000US-00632366.  
21-SEP-2000; 2000US-0234687P.  
27-SEP-2000; 2000US-0236359P.  
04-OCT-2000; 2000GB-00024263.  
(MOLE-) MOLECULAR DYNAMICS INC.  
Penn SG, Hanzel DK, Chen W, Rank DR;  
WPI; 2002-114183/15.  
Spatially-addressable set of single exon nucleic acid probes, used to  
measure gene expression in human lung samples.  
Claim 4; SEQ ID NO 17899; 634pp; English.  
The invention relates to a spatially-addressable set of single exon  
nucleic acid probes for measuring gene expression in a sample derived  
from human lung comprising single exon nucleic acid probes having one of  
12614 nucleic acid sequences mentioned in the specification, or their  
complements or the 12387 open reading frames derived from the 12614  
probes. Also included are a microarray comprising the novel set of probes  
; the novel set of probes which hybridize at high stringency to a nucleic  
acid expressed in the human lung; measuring gene expression in a sample  
derived from human lung, comprising (a) contacting the array with a  
collection of detectably labeled nucleic acids derived from human lung  
mRNA, and (b) measuring the label detectably bound to each probe of the  
array; identifying exons in a eukaryotic genome, comprising (a)  
algorithmically predicting at least one exon from genomic sequences of  
the eukaryote; and (b) detecting specific hybridization of detectably  
labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
having a fragment identical to the predicted exon, the probe is included  
in the above mentioned microarray; assigning exons to a single gene,  
comprising (a) identifying exons from genomic sequence by the method  
above and (b) measuring the expression of each of the exons in several  
tissues and/or cell types using hybridization to a single exon  
microarray having a probe with the exon, where a common pattern of  
expression of the exons in the tissues and/or cell types indicates that  
the exons should be assigned to a single gene; a peptide comprising one  
of 12011 sequences, mentioned in the specification, or encoded by the  
probes/open reading frames (ORF). The probes are used for gene expression  
analysis, and for identifying exons in a gene, particularly using human  
lung derived mRNA and for the study of lung diseases such as asthma, lung  
cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
tuberculous sclerotic, Gaucher's disease, Niemann-Pick disease, Hernandez-  
Pudlak syndrome, sarcoidosis, pulmonary haemolysis, pulmonary  
histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
Karsenger syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
present sequence is a single exon probe open reading frame of the

CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [http://wipo.int/publ/published\\_pct\\_sequences](http://wipo.int/publ/published_pct_sequences)  
XX

XX Sequence 88 BP; 27 A; 24 C; 12 G; 25 T; 0 U; 0 Other;  
SQ

Query Match 88.2%; Score 15; DB 6; Length 88;  
Best Local Similarity 60.0%; Pred. No. 7.8e+02;  
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCUGAUVUUCAGUCA 15  
Db 63 CCTGATTTCATTGCA 77

RESULT 9  
ABK61041  
ID ABK61041 standard; DNA; 15 BP.  
XX  
XX ABK61041;  
AC  
XX 02-JUL-2002 (first entry)  
DT  
XX  
XX Human CLCA1 gene enzymatic nucleic acid #5412.  
DE  
XX  
XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
KW  
XX antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
KW  
XX chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
KW  
XX oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
KW  
XX acetylcysteine.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200211674-A2.  
PN  
XX  
XX 14-FEB-2002.  
PD  
XX  
XX 09-AUG-2001; 2001WO-US024970.  
PF  
XX  
XX 09-AUG-2000; 2000US-0224383P.  
PR  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (SYNT) SYNTEX USA LLC.  
XX (THOM/) THOMPSON J.  
PA  
XX  
XX Thompson J, Mcswigen J, McKenzie T, Ayers D, Szymkowski DE;  
PI Grupe A;  
XX  
XX WPI; 2002-217145/27.  
DR  
XX  
XX Enzymatic polynucleotide that down regulates expression of chloride  
PT channel calcium activated gene, useful for treating Chronic obstructive  
PT pulmonary disease (COPD), chronic bronchitis and asthma.  
XX  
XX Claim 4; Page 138; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down  
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
CC useful as pharmaceutical agents for treating conditions such as chronic  
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
CC that are related to or will respond to the levels of CLCA1 in a cell or  
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
CC hence, are useful for treatment of a patient having a condition  
CC associated with the level of CLCA1, where the invention further comprises  
CC the use of one or more therapies under conditions suitable for the  
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
CC nucleic acids of the invention are also used as diagnostic tools to  
CC examine genetic drift and mutations within diseased cells or to detect  
CC the presence of CLCA1 RNA in a cell. This sequence represents an  
CC enzymatic nucleic acid molecule of the invention

XX  
SQ Sequence 15 BP; 2 A; 4 C; 2 G; 7 T; 0 U; 0 Other;  
XX

Query Match 82.4%; Score 14; DB 6; Length 15;  
Best Local Similarity 57.1%; Pred. No. 2.2e+03;  
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCUGAUVUUCAGUCA 14  
Db 2 CCTGATTTCATTGC 15

RESULT 10  
ABK5773  
ID ABK5773 standard; RNA; 17 BP.  
XX  
XX ABK5773;  
AC  
XX 02-JUL-2002 (first entry)  
DT  
XX  
XX Human CLCA1 gene enzymatic nucleic acid #144.  
DE  
XX  
XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
KW  
XX antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
KW  
XX chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
KW  
XX oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
KW  
XX acetylcysteine.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200211674-A2.  
PN  
XX  
XX 14-FEB-2002.  
PD  
XX  
XX 09-AUG-2001; 2001WO-US024970.  
PF  
XX  
XX 09-AUG-2000; 2000US-0224383P.  
PR  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (SYNT) SYNTEX USA LLC.  
XX (THOM/) THOMPSON J.  
PA  
XX  
XX Thompson J, Mcswigen J, McKenzie T, Ayers D, Szymkowski DE;  
PI Grupe A;  
XX  
XX WPI; 2002-217145/27.  
DR  
XX  
XX Enzymatic polynucleotide that down regulates expression of chloride  
PT channel calcium activated gene, useful for treating Chronic obstructive  
PT pulmonary disease (COPD), chronic bronchitis and asthma.  
XX  
XX Claim 4; Page 55; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down  
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
CC useful as pharmaceutical agents for treating conditions such as chronic  
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
CC that are related to or will respond to the levels of CLCA1 in a cell or  
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
CC hence, are useful for treatment of a patient having a condition  
CC associated with the level of CLCA1, where the invention further comprises  
CC the use of one or more therapies under conditions suitable for the  
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
CC nucleic acids of the invention are also used as diagnostic tools to  
CC examine genetic drift and mutations within diseased cells or to detect  
CC the presence of CLCA1 RNA in a cell. This sequence represents an  
CC enzymatic nucleic acid molecule of the invention

XX Sequence 17 BP; 6 A; 2 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 82.4%; Score 14; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 4 GAUUCAUUGCAGG 17  
1 GAUUCAUUGCAGG 14

RESULT 11  
ADG70258/C  
ID ADG70258 standard; DNA; 19 BP.  
AC ADG70258;  
XX  
XX  
DT 11-MAR-2004 (first entry)  
XX  
XX  
DE CLD8 exon 12 and ANGE exon 3 SNP identification primer #74.  
XX  
XX  
KW ANGE; CLD8; CLD7; ANGE-CLD8; ANGE-CLD7; CLD7-CLD8;  
KW ANGE-CLD8-CLD7; anti-allergic; anti-asthmatic; dermatological;  
KW antipruritic; anti-inflammatory; gene therapy; Ige-mediated disease;  
KW primer; ss.  
XX  
XX  
OS Unidentified.  
XX  
XX  
PN WO200300727-A2.  
XX  
XX  
PD 03-JAN-2003.  
XX  
XX  
PF 21-JUN-2002; 2002WO-GB002859.  
XX  
XX  
PR 21-JUN-2001; 2001GB-00015211.  
PR 21-JUN-2001; 2001GB-00015212.  
PR 21-JUN-2001; 2001GB-00015213.  
XX  
XX  
PA (ISIS-) ISIS INNOVATIONS LTD.  
PI Zhang Y, Moffatt M, Cookson W, Tinsley J;  
DR WPI; 2003-201405/19.  
XX  
XX  
PT New nucleic acid sequence comprising an ANGE, CLD8 or CLD7 mRNA, or  
PT their hybrid, useful for screening agents for treating Ige-mediated  
PT diseases, e.g. asthma, atopy, hay fever, eczema, atopic dermatitis, or  
PT allergic rhinitis.  
XX  
XX  
PS Disclosure; Page 408; 429pp; English.  
XX  
XX  
CC The invention relates to a novel isolated or recombinant nucleic acid  
CC sequence comprising an ANGE, CLD8 or CLD7 mRNA, or ANGE-CLD8, ANGE-  
CC CLD7, CLD7-CLD8, or ANGE-CLD8-CLD7 hybrid mRNA sequence, its  
CC complement, homologue or fragment. The novel nucleic acid sequences have  
CC the following activities: anti-allergic, anti-asthmatic, dermatological,  
CC antipruritic, and anti-inflammatory. The nucleic acids of the invention may  
CC be used in gene therapy to treat disorders. The nucleic acid sequences  
CC are useful for screening agents that inhibit or enhance activity of an  
CC ANGE, CLD8 or CLD7 gene. The agent or antibody is useful for treating  
CC Ige-mediated diseases, such as asthma, atopy, hay fever, eczema, atopic  
CC dermatitis, allergic rhinitis or non-atopic asthma. The antibody is  
CC useful in an assay detecting or measuring the polypeptide in the sample.  
CC The host cell is useful for producing, regulating and analyzing the  
CC polypeptide. The splice variant of ANGE, CLD8, or CLD7 is useful for  
CC diagnosing an Ige-mediated disease, atopy, a form of atopic disease or  
CC non-atopic asthma, or predicting the severity, or predisposition to a  
CC disease. This polynucleotide sequence represents a primer used in the  
CC exemplification of the invention.  
XX  
XX  
SQ Sequence 19 BP; 7 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 82.4%; Score 14; DB 10; Length 19;  
Best Local Similarity 64.3%; Pred. No. 2.2e+03;  
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Query Match 82.4%; Score 14; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 4 GAUUCAUUGCAGG 17  
1 GAUUCAUUGCAGG 14

RESULT 12  
ACCT0300  
ID ACCT0300 standard; DNA; 22 BP.  
AC ACCT0300;  
XX  
XX  
DT 11-AUG-2003 (first entry)  
XX  
XX  
DE PCR primer used to isolate cDNA encoding the human mucinase AMCase.  
XX  
XX  
KW Human; mucinase; AMCase; mucin; enzyme; chitin; cystic fibrosis;  
KW chronic obstructive pulmonary disease; asthma; bronchitis; PCR;  
KW tuberculosis; mucin-producing tumour; protozoan parasite; primer; ss.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO2003038079-A2.  
XX  
XX  
PD 08-MAY-2003.  
XX  
XX  
PF 01-NOV-2002; 2002WO-NL000694.  
XX  
XX  
PR 02-NOV-2001; 2001US-00004219.  
XX  
XX  
PA (MACR-) MACROZYME BV.  
XX  
XX  
PI Aerts JMF, Boot RG;  
DR WPI; 2003-457394/43.  
XX  
XX  
PT New recombinant and/or isolated or purified mammalian mucinase or its  
PT modified form, useful for diagnosing, preventing or treating diseases in  
PT which mucus is involved, e.g. cystic fibrosis, comprises a mucin-  
PT hydrolyzing activity.  
XX  
XX  
PS Example 1; Page 33; 77pp; English.  
XX  
XX  
CC PCR primers ACCT0299-ACCT0301 were used to isolate cDNA encoding a human  
CC mucinase, designated AMCase. This enzyme hydrolyses a mucin. The mucinase  
CC is useful in the treatment of a subject against a disease in which mucus  
CC is involved or against infection by a chitin-containing pathogen. The  
CC mucinase is useful in diagnosing, preventing or treating diseases in  
CC which mucus is involved, such as cystic fibrosis, chronic obstructive  
CC pulmonary disease, asthma, bronchitis, tuberculosis, a mucin-producing  
CC tumour, or infection by a protozoan parasite  
XX  
XX  
SQ Sequence 22 BP; 4 A; 3 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 78.8%; Score 13.4; DB 9; Length 22;  
Best Local Similarity 53.3%; Pred. No. 4.6e+03;  
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
DB 2 CUGAUUCAUUGCAG 16  
8 CUGAUUCAUUGCAG 22

RESULT 13  
ADG16067/C  
ID ADG16067 standard; DNA; 52 BP.  
AC ADG16067;  
XX  
XX  
DT 26-FEB-2004 (first entry)  
XX  
XX  
DE PQGDH mutagenic PCR primer SEQ ID NO:17.  
XX

KW modified pyrroloquinoline quinone dependent glucose dehydrogenase;  
KM pyrroloquinoline quinone dependent glucose dehydrogenase;  
KM modified PQQGDH; PQQGDH; enzyme; glucose; clinical assay; food analysis;  
KM Acinetobacter baumannii; mutagenesis; PCR primer; ss.  
OS Synthetic.  
OS Acinetobacter baumannii.  
PN EPI367120-A2.  
XX  
PD 03-DEC-2003.  
XX  
PF 27-MAY-2003; 2003BP-00011930.  
XX  
PR 27-MAY-2002; 2002JP-00152911.  
XX  
PR 27-MAY-2002; 2002JP-00152913.  
XX  
PR 24-MAR-2003; 2003JP-00080244.  
XX  
PR 24-MAR-2003; 2003JP-00080310.  
XX  
PA (TOYM ) TOYO BOSEKI KK.  
XX  
PI Takeshima S, Sogabe A, Oka M;  
XX  
DR WPI; 2004-063970/07.  
XX  
XX New modified pyrroloquinoline dependent glucose dehydrogenase having less  
PT activity on disaccharides and/or greater stability than wild-type PQQGDH,  
PT for measuring glucose in clinical assay or food analysis.  
XX  
PS Example 5; SEQ ID NO 17; 45bp; English.  
XX  
CC The present invention describes a modified pyrroloquinoline quinone (PQQ)  
CC dependent glucose dehydrogenase (PQQGDH) having less activity on  
CC disaccharides and/or greater stability than wild-type PQQGDH. Also  
CC described: (1) a gene coding for the modified PQQGDH; (2) a vector  
CC containing the gene of (1); (3) a transformant transformed by the vector  
CC of (2); (4) a method of manufacturing a modified PQQGDH comprising  
CC culturing the transformant of (3); (5) a glucose assay kit comprising  
CC the modified PQQGDH; and (6) a method of determining glucose  
CC concentration in a sample using the modified PQQGDH. The modified PQQGDH  
CC is useful for measuring glucose in clinical assay or food analysis. The  
CC present sequence is used in the exemplification of the present invention.  
XX  
SQ Sequence 52 BP; 15 A; 6 C; 6 G; 16 T; 0 U; 9 Other;  
Query Match 78.8%; Score 13.4; DB 12; Length 52;  
Best Local Similarity 53.3%; Pred. No. 5e+03; 1; Indels 0; Gaps 0;  
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
QY 3 UGAAUUCAUUGCAGG 17  
Db 15 TGATTGTGATTCGACG 1  
RESULT 14  
AAT20442/C  
ID AAT20442 standard; cDNA to mRNA; 66 BP.  
XX  
AC AAT20442;  
XX  
DT 19-JUL-1996 (first entry)  
XX  
DE Human gene signature HUMGS01596.  
XX  
KM Gene signature; messenger RNA; mRNA; relative abundance; frequency;  
KM human; cloning; mapping; non-biased library; diagnosis; detection;  
KM cell typing; abnormal cell function; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9514772-A1.  
XX  
PD 01-JUN-1995.

XX  
PF 11-NOV-1994; 94WO-JP001916.  
XX  
PR 12-NOV-1993; 93JP-00355504.  
XX  
PA (MATS/) MATSUBARA K.  
XX  
PA (OKUBO/) OKUBO K.  
XX  
PI Matsubara K, Okubo K;  
XX  
DR WPI; 1995-206931/27.  
XX  
PT Single-stranded DNA for identifying gene signatures - isolated from 3'-  
PT directed human cDNA library that reflects relative abundance of corresp.  
PT mRNA in specific human tissues.  
XX  
PS Claim 1; Page 637; 2245pp; Japanese.  
XX  
CC A single-stranded DNA (or its complementary strand or the corresp. double  
CC -stranded DNA) which comprises one of the 7837 "GS" sequences given in  
CC AAT19001-726837 and which is able to hybridise to part of human genomic  
CC DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were  
CC obtained from 3'-directed cDNA libraries prepared from various human  
CC tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using  
CC poly(T) as the sole primer. Since the 3'-untranslated sequence is unique  
CC to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise  
CC with specific mRNAs. Each library is constructed so as to reflect  
CC accurately the relative abundance of different mRNAs in the particular  
CC tissue from which it was derived. The appearance frequency of a given GS  
CC in a cDNA library can be determined (esp. using primers and probes  
CC derived from the GS sequences) as a means of diagnosing abnormal cell  
CC function or for recognising different cell types  
XX  
SQ Sequence 66 BP; 18 A; 14 C; 8 G; 23 T; 0 U; 3 Other;  
Query Match 78.8%; Score 13.4; DB 2; Length 66;  
Best Local Similarity 53.3%; Pred. No. 5.1e+03; 1; Indels 0; Gaps 0;  
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
QY 3 UGAAUUCAUUGCAGG 17  
Db 54 TGATTGTGATTCGACG 40  
RESULT 15  
ABK61045  
ID ABK61045 standard; DNA; 15 BP.  
XX  
AC ABK61045;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE Human CLCA1 gene enzymatic nucleic acid #5416.  
XX  
KM Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
KM antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
KM chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
KM oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
KM acetylcysteine.  
XX  
OS Homo sapiens.  
XX  
PN WO200211674-A2.  
XX  
PD 14-FEB-2002.  
XX  
PR 09-AUG-2001; 2001WO-US024970.  
XX  
PF 09-AUG-2000; 2000US-0224383P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (SYNT) SYNTX USA LLC.  
PA (THOM/) THOMPSON J.



Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.

Claim 4, Page 111, 152pp, English.

The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention

Sequence 17 BP, 3 A, 5 C, 2 G, 0 T, 7 U, 0 Other;

Query Match 76.5%; Score 13; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 7.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCUGAUTCACUUG 13  
|||||  
5 CCUGAUTCACUUG 17

RESURF 18  
ADP97171/C  
ADP97171 standard; DNA, 43 BP.

ADP97171;  
23-SEP-2004 (first entry)

C. albicans specific gene,orf6.3991, knockout downstream primer.

Diploid fungal cell; allele; gene disruption cassette;  
promoter replacement fragment; antifungal; fungicide; gene therapy;  
infection; Candida albicans; knockout; primer; ss.

Candida albicans.  
Undefined.

WO2004056965-A2.

08-JUL-2004.

19-DEC-2003; 2003WO-US040618.

19-DEC-2002; 2002US-0434832P.

(ELIT-) ELITRA PHARM INC.  
(ELIT-) ELITRA CANADA LTD.

Roemer T, Jiang B, Boone C, Bussey H;  
WPI; 2004-500296/47.

Constructing a strain of diploid fungal cells in which both alleles of a gene are modified comprises modifying the alleles of a gene in the fungal cells by recombination using a gene disruption cassette and a promoter replacement fragment.

Claim 76; SEQ ID NO 1206; 163pp; English.

The invention relates to a novel method for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The method comprises modifying the alleles of a gene in diploid fungal cells by recombination using a gene disruption cassette and a promoter replacement fragment. The invention further comprises: assembling a collection of diploid fungal cells each of which comprises modified alleles of a different gene; a strain of diploid fungal cells comprising modified alleles of a gene, where the first allele of the gene is inactivated by a gene disruption cassette comprising a nucleotide sequence encoding an expressible selectable marker; and the expression of the second allele of the gene is regulated by a heterologous promoter that is operably linked to the coding region of the second allele of the gene, and where the gene encodes the polypeptide mentioned above; a collection of diploid fungal strains comprising the diploid strains cited above, where substantially all the different genes that encode the above amino acid sequences are modified and are present in different diploid strains in the collection; a nucleic acid molecule microarray comprising nucleic acid molecules, where each nucleic acid molecule comprises a nucleotide sequence that is hybridizable to a target nucleotide sequence comprising any of the 310 nucleotide sequences listed in the specification (ADP98516-ADP98825); identifying a gene that is essential to the survival or growth of a fungus, that contributes to the virulence and/or pathogenicity of a fungus, or that contributes to the resistance of a diploid fungus to an antifungal agent; identifying an antifungal agent that inhibits the growth of a diploid fungus, or a therapeutic agent for treatment of a mammalian disease; correlating changes in the levels of proteins or gene transcripts with the inhibition of growth or proliferation of a diploid fungal cell; a purified or isolated nucleic acid molecule comprising a nucleotide sequence encoding a gene product required for proliferation of Candida albicans, where the gene product consists of any of the above-mentioned amino acid sequences; a vector comprising a promoter operably linked to the nucleic acid molecule cited above; a host cell containing the vector; a purified or isolated polypeptide comprising any of the 61 amino acid sequences given in the specification (ADP96778-ADP96778); a fusion protein comprising a fragment of a first polypeptide fused to a second polypeptide, the fragment consisting of at least 6 consecutive residues of any of ADP98826-ADP99135; producing a polypeptide; identifying a compound which modulates the activity of a gene product encoded by a nucleic acid comprising any of ADP98516-ADP98825; eliciting an immune response in an animal; a strain of Candida albicans, where a first allele of a gene comprising any of ADP98516-ADP98825 is inactive and a second allele of the gene is under the control of a heterologous promoter; identifying a compound or binding partner that binds to the polypeptide comprising any of ADP98826-ADP99135, or its fragment; identifying a compound having the ability to inhibit growth or proliferation of Candida albicans; inhibiting growth or proliferation of Candida albicans cells; manufacturing an antipneumonic compound; treating an infection of a subject by Candida albicans; preventing or containing contamination of an object by Candida albicans, or for preventing or inhibiting formation on a surface of a biofilm comprising Candida albicans; a pharmaceutical composition comprising a therapeutic amount of an agent which reduces the activity or level of a gene product encoded by a nucleic acid comprising any of ADP98516-ADP98825 in a pharmaceutical carrier; an antibody preparation which binds the polypeptide; methods for evaluating a compound against a target gene product encoded by any of ADP98516-ADP98825; identifying an antimycotic compound; a computer or a computer readable medium that comprises at least one of the nucleotide sequences mentioned in the specification or at least one amino acid sequence selected from ADP98826-ADP99135; a method assisted by a computer for identifying a putatively essential gene of a fungus; and a protein array comprising proteins, where at least one protein comprises an amino acid sequence or a portion of an amino acid sequence selected from ADP98516-ADP98825. The novel methods and compositions have fungicide activity. The compositions may be used in gene therapy. The composition and methods are useful for drug screening purposes or for diagnosing, preventing or treating infections associated with Candida albicans. These may also be used for constructing strains useful for identification and validation of gene products as effective targets for therapeutic intervention, for identifying and validating gene products as effective targets for therapeutic intervention, and for collecting identified essential genes. This polynucleotide sequence represents a knockout primer used in the exemplification of the



XX AAV51602;  
AC  
XX 02-FEB-1999 (first entry)  
DT  
XX Zea mays genome forward PCR primer #202.  
DE  
XX Polymorphic marker; allele-specific; probe; amplification; PCR primer;  
XX hybridisation; plant; hybrid certification; genetic contribution;  
KM progeny; back-cross; hybrid; ancestry; corn; ss.  
XX  
OS Synthetic.  
OS Zea mays.  
PN WO9824796-A1.  
XX  
PD 11-JUN-1998.  
XX  
PF 01-DEC-1997; 97WO-US021782.  
XX  
PR 02-DEC-1996; 96US-0032069P.  
PR 07-MAR-1997; 97US-00813507.  
XX  
PA (AFRY-) AFFYMETRIX INC.  
XX  
PI Lemieux B, Landry BS, Sapolsky RJ, Murigneux A;  
DR WPI; 1998-333252/29.  
XX  
XX Braasia species allele-specific oligonucleotide probes and primers -  
PT useful for plant breeding.  
XX  
PS Example 1; Page 53; 65pp; English.  
XX  
CC AAV51401-US1704 are forward PCR primers used to amplify fragments of the  
CC Zea mays genome in order to detect polymorphic markers. Such markers can  
CC be used in the construction of allele-specific primers and probes for  
CC amplification or hybridisation, e.g. to determine common or disparate  
CC ancestry between 2 or more plants, to monitor the genetic contribution of  
CC an ancestral plant, to trace the progeny of proprietary plants, in  
CC certification of a hybrid plant or to identify the progeny of a back-  
CC crossed plant with an ancestral plant  
CC  
SQ Sequence 23 BP; 5 A; 5 C; 5 G; 8 T; 0 U; 0 Other;  
Query Match 75.3%; Score 12.8; DB 2; Length 23;  
Best Local Similarity 56.2%; Pred. No. 9.5e+03;  
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CCUGAUUUCAUUGCAG 16  
DB 5 CTTGATTCATTCGACG 20  
RESULT 22  
ACK08857  
ID ACK08857 standard; DNA; 25 BP.  
XX  
AC ACK08857;  
DT 14-OCT-2003 (first entry)  
XX  
DE Human microarray DNA oligonucleotide SEQ ID NO 108838.  
XX  
KM EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KM genetic variation; diallelic marker; polymorphism; human;  
KM cross-species comparison.  
XX  
XX Homo sapiens.  
OS  
PN US2003104410-A1.  
XX  
PD 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.  
PF  
XX 16-MAR-2001; 2001US-0276759P.  
PR  
XX (AFRY-) AFFYMETRIX INC.  
PA  
XX Miltmann MP;  
XX WPI; 2003-567953/53.  
DR  
XX New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-plot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
XX  
PS Claim 1; SEQ ID NO 108838; 9pp; English.  
XX  
CC The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying diallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 25 BP; 9 A; 5 C; 4 G; 7 T; 0 U; 0 Other;  
Query Match 75.3%; Score 12.8; DB 9; Length 25;  
Best Local Similarity 56.2%; Pred. No. 9.5e+03;  
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CCUGAUUUCAUUGCAG 16  
DB 9 CCAGATTTCATTCGAG 24  
RESULT 23  
ABK33718/C  
ID ABK33718 standard; DNA; 32 BP.  
XX  
AC ABK33718;  
DT 08-MAY-2002 (first entry)  
XX  
DE S. pneumoniae BVH-3 gene, PCR primer HAMJ 359.  
XX  
KM BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia; pneumonia;  
KM streptococcal bacterial infection; PCR; primer; ss.  
XX  
OS Streptococcus pneumoniae.  
PN WO200198334-A2.  
XX  
PD 27-DEC-2001.  
XX  
PF 19-JUN-2001; 2001WO-CA000908.

PR 20-JUN-2000; 2000US-0212683P.  
 XX (SHIR-) SHIRE BIOCHEM INC.  
 XX  
 XX Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;  
 PI WPI; 2002-122272/16.  
 XX  
 XX New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing  
 PT polypeptides, useful as vaccine components for treating or preventing  
 PT streptococcal infections such as otitis media, meningitis, and  
 PT bacteraemia.  
 XX  
 XX Example 1; Page 33; 113pp; English.  
 PS  
 XX The invention describes an isolated polypeptide (I) with 70-90% identity  
 CC to Streptococcus pneumonia protein BVH-3, BVH-11, variance of BVH-3 or  
 CC BVH-11, or chimeric sequences derived from them. A vaccine (II)  
 CC comprising (I) is useful for therapeutic or prophylactic treatment of  
 CC meningitis, otitis media, bacteraemia or pneumonia infection in an  
 CC individual susceptible to these disorders. (II) is also useful for  
 CC therapeutic or prophylactic treatment of any streptococcal bacterial  
 CC infection (e.g., caused by Streptococcus pneumoniae, group A  
 CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such  
 CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nodocidia or  
 CC Staphylococcus aureus) in an individual susceptible to the infection. A  
 CC polynucleotide (III) encoding (I) is useful in DNA immunisation.  
 CC techniques. The Streptococcus polypeptides are useful in a diagnostic  
 CC test for S. pneumoniae infection. (III) is useful for designing DNA  
 CC probes for use in detecting the presence of Streptococcus in a biological  
 CC sample suspected of containing the bacteria. The DNA probes may also be  
 CC used for detecting circulating S. pneumonia nucleic acid in a sample for  
 CC diagnosing streptococcal infections. This sequence represents a primer  
 CC used for the isolation of S. pneumoniae genes from which the antigenic  
 CC peptides of the invention are derived  
 XX  
 SQ Sequence 32 BP; 9 A; 10 C; 6 G; 7 T; 0 U; 0 Other;  
 Query Match 75.3%; Score 12.8; DB 6; Length 32;  
 Best Local Similarity 56.2%; Pred. No. 9.8e+03;  
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 OY 2 CUGAUVUUCAGCAG 17  
 DB 24 CTGATTTCATGCGG 9  
 RESULT 24  
 AAV50992  
 ID AAV50992 standard; DNA; 41 BP.  
 XX  
 AC AAV50992;  
 XX  
 DT 04-JAN-1999 (first entry)  
 XX  
 DE Maize polymorphic marker S43G1/G4-1 DNA.  
 XX  
 XX Polymorphic marker; allele-specific; primer; probe; amplification;  
 KW hybridisation; plant; hybrid certification; genetic contribution;  
 KW progeny; back-cross; hybrid; ancestry; maize; ss.  
 XX  
 OS Zea mays.  
 XX  
 XX Key Location/Qualifiers  
 FT variation 21  
 FT /\*tag= a  
 FT /replace= a  
 FT /note= "polymorphism"  
 XX  
 PN WO9824796-A1.  
 XX 11-JUN-1998.  
 XX

PF 01-DEC-1997; 97WO-US021782.  
 XX  
 XX 02-DEC-1996; 96US-0032069P.  
 PR 07-MAR-1997; 97US-00813507.  
 XX  
 XX (AFFY-) AFFYMETRIX INC.  
 PA  
 XX Lemieux B, Landry BS, Sapolsky RJ, Murgineux A;  
 PI WPI; 1998-333252/29.  
 XX  
 XX Brassica species allele-specific oligonucleotide probes and primers -  
 PT useful for plant breeding.  
 XX  
 XX Claim 1; Page 43; 65pp; English.  
 PS  
 XX This DNA sequence is a region of a Zea mays genome which contains a  
 CC polymorphic marker. This sequence can be used in the construction of  
 CC allele-specific primers and probes for amplification or hybridisation,  
 CC e.g. to determine common or disparate ancestry between 2 or more plants,  
 CC to monitor the genetic contribution of an ancestral plant, to trace the  
 CC progeny of proprietary plants, in certification of a hybrid plant or to  
 CC identify the progeny of a back-crossed plant with an ancestral plant  
 CC  
 XX  
 SQ Sequence 41 BP; 9 A; 10 C; 14 G; 8 T; 0 U; 0 Other;  
 Query Match 75.3%; Score 12.8; DB 2; Length 41;  
 Best Local Similarity 56.2%; Pred. No. 1e+04;  
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 CUGAUVUUCAGCAG 16  
 DB 1 CTGATTTCATGCGG 16  
 RESULT 25  
 AAV50971  
 ID AAV50971 standard; DNA; 41 BP.  
 XX  
 AC AAV50971;  
 XX  
 DT 04-JAN-1999 (first entry)  
 XX  
 DE Maize polymorphic marker S43G2/G6-2B DNA.  
 XX  
 XX Polymorphic marker; allele-specific; primer; probe; amplification;  
 KW hybridisation; plant; hybrid certification; genetic contribution;  
 KW progeny; back-cross; hybrid; ancestry; maize; ss.  
 XX  
 OS Zea mays.  
 XX  
 XX Key Location/Qualifiers  
 FT variation 21  
 FT /\*tag= a  
 FT /replace= g  
 FT /note= "polymorphism"  
 XX  
 PN WO9824796-A1.  
 XX 11-JUN-1998.  
 XX  
 PD 01-DEC-1997; 97WO-US021782.  
 XX  
 XX 02-DEC-1996; 96US-0032069P.  
 PR 07-MAR-1997; 97US-00813507.  
 XX  
 XX (AFFY-) AFFYMETRIX INC.  
 PA  
 XX Lemieux B, Landry BS, Sapolsky RJ, Murgineux A;  
 PI WPI; 1998-333252/29.  
 XX  
 XX Brassica species allele-specific oligonucleotide probes and primers -  
 PT



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AAV47798
ID AAV47798 standard; DNA; 41 BP.
XX
AC AAV47798;
XX
DT 27-AUG-2003 (revised)
DT 14-OCT-1998 (first entry)
XX
DE Maize polymorphic site oligonucleotide marker Wx1-G2/G6-2B.
XX
KM Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;
KM polymorphic site; corn; gramineae species; ss.
XX
OS Synthetic.
OS Zea.
XX
PN WO9830717-A2.
XX
PD 16-JUL-1998.
XX
PF 02-DEC-1997; 97WO-EP007134.
XX
PR 02-DEC-1996; 96US-0032069P.
XX
PA (BIOC-) BIOCEM SA.
XX
PI Murigneux A;
XX
DR WPI; 1998-399160/34.
XX
PT Vegetal sequences including single nucleotide polymorphism - useful, e.g.
PT to determine polymorphisms in plants, determine strain in plant breeding
PT and to correlate polymorphisms with phenotypic traits.
XX
PS Claim 2; Page 13; 32pp; English.
XX
CC The present invention describes a nucleic acid segment comprising at
CC least 10 contiguous nucleotides from a vegetal sequence including a
CC polymorphic site which is a single nucleotide polymorphism (SNP), or the
CC complement of the segment. Also described are: (1) an allele-specific
CC oligonucleotides hybridising to segment, or their complements, and (2) a
CC method of analysing nucleic acids from a subject, by determining if a
CC base is occupying any one (or a set) of polymorphic sites in 261
CC sequences derived from six maize lines (see AAV47701 to AAV47961). The
CC segments are useful in fingerprint analysis in plants to determine which
CC polymorphisms are present, which strain a plant belongs to and to
CC distinguish between strains. The polymorphisms may correlate with
CC phenotypic traits (e.g. plant growth rate or crop yield), and the
CC segments are useful to determine the presence/absence of specific
CC polymorphisms correlating with the existence/absence of particular
CC traits. The segments are also useful in marker assisted back-cross
CC techniques to select plants with a higher percentage of recurrent parent
CC in a back-cross population. Segments incorporate SNPs which occur more
CC frequently than other polymorphism types and are therefore more likely to
CC be located close to genetic loci of interest; different forms of
CC characterised SNPs are also often easier to detect than other
CC polymorphism types. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 41 BP; 9 A; 10 C; 13 G; 8 T; 0 U; 1 Other;

Query Match          75.3%; Score 12.8; DB 2; Length 41;
Best Local Similarity 56.2%; Pred. No. 1e+04;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAUUGCG 16
   | : || : || : || |
DB 1 CTTGATTGCATTGCG 16

RESULT 29
AAV47809
ID AAV47809 standard; DNA; 41 BP.

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```

AC AAV47809;
XX
DT 27-AUG-2003 (revised)
DT 14-OCT-1998 (first entry)
XX
DE Maize polymorphic site oligonucleotide marker Wx1-G1/G4-1.
XX
KM Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;
KM polymorphic site; corn; gramineae species; ss.
XX
OS Synthetic.
OS Zea.
XX
PN WO9830717-A2.
XX
PD 16-JUL-1998.
XX
PF 02-DEC-1997; 97WO-EP007134.
XX
PR 02-DEC-1996; 96US-0032069P.
XX
PA (BIOC-) BIOCEM SA.
XX
PI Murigneux A;
XX
DR WPI; 1998-399160/34.
XX
PT Vegetal sequences including single nucleotide polymorphism - useful, e.g.
PT to determine polymorphisms in plants, determine strain in plant breeding
PT and to correlate polymorphisms with phenotypic traits.
XX
PS Claim 2; Page 13; 32pp; English.
XX
CC The present invention describes a nucleic acid segment comprising at
CC least 10 contiguous nucleotides from a vegetal sequence including a
CC polymorphic site which is a single nucleotide polymorphism (SNP), or the
CC complement of the segment. Also described are: (1) an allele-specific
CC oligonucleotides hybridising to segment, or their complements, and (2) a
CC method of analysing nucleic acids from a subject, by determining if a
CC base is occupying any one (or a set) of polymorphic sites in 261
CC sequences derived from six maize lines (see AAV47701 to AAV47961). The
CC segments are useful in fingerprint analysis in plants to determine which
CC polymorphisms are present, which strain a plant belongs to and to
CC distinguish between strains. The polymorphisms may correlate with
CC phenotypic traits (e.g. plant growth rate or crop yield), and the
CC segments are useful to determine the presence/absence of specific
CC polymorphisms correlating with the existence/absence of particular
CC traits. The segments are also useful in marker assisted back-cross
CC techniques to select plants with a higher percentage of recurrent parent
CC in a back-cross population. Segments incorporate SNPs which occur more
CC frequently than other polymorphism types and are therefore more likely to
CC be located close to genetic loci of interest; different forms of
CC characterised SNPs are also often easier to detect than other
CC polymorphism types. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 41 BP; 9 A; 10 C; 13 G; 8 T; 0 U; 1 Other;

Query Match          75.3%; Score 12.8; DB 2; Length 41;
Best Local Similarity 56.2%; Pred. No. 1e+04;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAUUGCG 16
   | : || : || : || |
DB 1 CTTGATTGCATTGCG 16

RESULT 30
AAV47788
ID AAV47788 standard; DNA; 41 BP.
XX
AC AAV47788;
XX
DT 27-AUG-2003 (revised)

```

DT 14-OCT-1998 (first entry)  
DE Maize polymorphic site oligonucleotide marker Wx1-G2/G6-2B.  
XX  
KW Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;  
KM polymorphic site; corn; gramineae species; ss.  
XX  
OS Synthetic.  
XX Zea.  
XX  
PN WO9830717-A2.  
XX  
PD 16-JUL-1998.  
XX  
PF 02-DEC-1997; 97WO-EP0071134.  
XX  
PR 02-DEC-1996; 96US-0032069P.  
XX  
PA (BIOC-) BIOCEM SA.  
XX  
PI Murgineux A;  
XX  
DR WPI, 1998-399160/34.  
XX  
PT Vegetal sequences including single nucleotide polymorphism - useful, e.g.  
PT to determine polymorphisms in plants, determine strain in plant breeding  
PT and to correlate polymorphisms with phenotypic traits.  
XX  
PS Claim 2; Page 13; 32pp; English.  
XX  
CC The present invention describes a nucleic acid segment comprising at  
CC least 10 contiguous nucleotides from a vegetal sequence including a  
CC polymorphic site which is a single nucleotide polymorphism (SNP), or the  
CC complement of the segment. Also described are: (1) an allele-specific  
CC oligonucleotides hybridising to segment, or their complements, and (2) a  
CC method of analysing nucleic acids from a subject, by determining if a  
CC base is occupying any one (or a set) of polymorphic sites in 261  
CC sequences derived from six maize lines (see AAV47701 to AAV47961). The  
CC segments are useful in fingerprint analysis in plants to determine which  
CC polymorphisms are present, which strain a plant belongs to and to  
CC distinguish between strains. The polymorphisms may correlate with  
CC phenotypic traits (e.g. plant growth rate or crop yield), and the  
CC segments are useful to determine the presence/absence of specific  
CC polymorphisms correlating with the existence/absence of particular  
CC traits. The segments are also useful in marker assisted back-cross  
CC techniques to select plants with a higher percentage of recurrent parent  
CC in a back-cross population. Segments incorporate SNPs which occur more  
CC frequently than other polymorphism types and are therefore more likely to  
CC be located close to genetic loci of interest; different forms of  
CC characterised SNPs are also often easier to detect than other  
CC polymorphism types. (Updated on 27-AUG-2003 to correct OS field.)  
XX  
SQ Sequence 41 BP; 9 A; 10 C; 13 G; 8 T; 0 U; 1 Other;  
XX  
Query Match 75.3%; Score 12.8; DB 2; Length 41;  
Best Local Similarity 56.2%; Pred. No. 1e+04;  
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
OY 1 CCUGAUUUCAUUUCGAG 16  
DB 1 CTGATTTCATTTCGAG 16  
XX  
RESULT 31  
ID AAH86424/c  
AAH86424 standard; DNA; 63 BP.  
XX  
AC AAH86424;  
XX  
DT 27-FEB-2002 (first entry)  
XX  
DE Human single nucleotide polymorphism containing DNA sequence #1281.  
XX

KW Biallelic marker; polymorphism; human; disease; diagnosis; treatment;  
KW phenotypic trait; gene therapy; forensic; paternity; mapping; cancer;  
KM transgenic; single nucleotide polymorphism; SNP; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FH Location/Qualifiers  
FT variation  
FT replace(20,C)  
FT /\*tag= a  
FT /standard\_name= "single nucleotide polymorphism"  
XX  
PN WO9953095-A2.  
XX  
PD 21-OCT-1999.  
XX  
PF 30-MAR-1999; 99WO-US006893.  
XX  
PR 09-APR-1998; 98US-00057871.  
XX  
PA (WHEB ) WHITEHEAD INST BIOMEDICAL RES.  
XX  
PI Lander ES, Wang D, Hudson T;  
XX  
DR WPI, 1999-620443/53.  
XX  
PT Polymorphic human genomic sequences and related allele-specific probes  
PT and primers, useful for genetic analysis, e.g. diagnosis and monitoring  
PT of disease.  
XX  
PS Claim 1; Page 168; 330pp; English.  
XX  
CC This invention describes novel human nucleic acid segments (I) containing  
CC polymorphic sites. The polymorphisms (or disease susceptibility) or other  
CC correlating disease polymorphisms (or disease susceptibility) or other  
CC phenotypic traits (e.g. baldness, obesity, fertility, strength, response  
CC to drugs etc.); diagnosing and monitoring e.g. cancer, inflammation,  
CC heart or central nervous system diseases; detecting susceptibility to  
CC microbial infection; treating or preventing such diseases; forensic  
CC analysis; gene therapy; paternity testing; mapping genomic loci  
CC associated with phenotypic traits (and subsequent cloning of the genes  
CC responsible); and the production of transgenic organisms. Antibodies  
CC raised against (I) are useful as diagnostic and therapeutic tools and in  
CC drug screening. AAH85144 - AAH87644 represent the human DNA sequences  
CC containing biallelic polymorphic sites described in the invention  
XX  
SQ Sequence 63 BP; 18 A; 17 C; 7 G; 21 T; 0 U; 0 Other;  
XX  
Query Match 75.3%; Score 12.8; DB 2; Length 63;  
Best Local Similarity 50.0%; Pred. No. 1e+04;  
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;  
OY 2 CCUGAUUUCAUUUCGAG 17  
DB 49 CTGTTTCATTTCGAG 34  
XX  
RESULT 32  
ID AA127809/c  
AA127809 standard; DNA; 80 BP.  
XX  
AC AA127809;  
XX  
DT 12-OCT-2001 (first entry)  
XX  
DE Probe #17742 for gene expression analysis in human cervical cell sample.  
XX  
KM Probe; human; microarray; gene expression; cervical epithelial cell;  
KM cervical cancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157278-A2.  
XX

PD 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US000670.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI: 2001-488901/53.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
XX gene expression in human cervical epithelial cells.  
XX  
PS Claim 25; SEQ ID NO 17742; 487bp; English.  
XX  
CC The present invention relates to human single exon nucleic acid probes  
CC (SENPs). The present sequence is one such probe. The SENPs are derived  
CC from human HeLa cells. The SENPs can be used to produce a single exon  
CC microarray, which can be used for measuring human gene expression in a  
CC sample derived from human cervical epithelial cells. By measuring gene  
CC expression, the probes are therefore useful in grading and/or staging of  
CC diseases of the cervix, notably cervical cancer. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;  
XX  
Query Match 75.3%; Score 12.8; DB 4; Length 80;  
Best Local Similarity 56.2%; Pred. No. 1.1e+04;  
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CUGAUNUCANUGCAGG 17  
Db |||::|||::|||  
57 CTGATTGCATTTCAGG 42  
XX  
RESULT 33  
ABA76122/C  
ID ABA76122 standard; DNA; 80 BP.  
XX  
AC ABA76122;  
XX  
DT 01-FEB-2002 (first entry)  
XX  
DE Human foetal liver single exon nucleic acid probe #24427.  
XX  
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157277-A2.  
XX  
PD 09-AUG-2001.  
XX  
PE 30-JAN-2001; 2001WO-US000669.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX

PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI: 2001-483447/52.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
XX gene expression in human fetal liver.  
XX  
PS Claim 4; SEQ ID NO 24427; 639pp + Sequence Listing; English.  
XX  
CC The invention relates to a single exon nucleic acid probe for measuring  
CC human gene expression in a sample derived from human foetal liver. The  
CC single exon nucleic acid probes may be used for predicting, measuring and  
CC displaying gene expression in samples derived from human fetal liver. The  
CC present sequence is a single exon nucleic acid probe of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;  
XX  
Query Match 75.3%; Score 12.8; DB 4; Length 80;  
Best Local Similarity 56.2%; Pred. No. 1.1e+04;  
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CUGAUNUCANUGCAGG 17  
Db |||::|||::|||  
57 CTGATTGCATTTCAGG 42  
XX  
RESULT 34  
AA156782/C  
ID AA156782 standard; DNA; 80 BP.  
XX  
AC AA156782;  
XX  
DT 17-OCT-2001 (first entry)  
XX  
DE Probe #25468 used to measure gene expression in human placenta sample.  
XX  
KW Probe; microarray; human; placenta; antenatal diagnosis;  
XX genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157272-A2.  
XX  
PD 09-AUG-2001.  
XX  
PE 30-JAN-2001; 2001WO-US000663.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI: 2001-488897/53.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
XX gene expression in human placenta.  
XX  
PS Claim 25; SEQ ID NO 25468; 654pp; English.  
XX  
CC The present invention relates to single exon nucleic acid probes (SENPs).  
CC The present sequence is one such probe. The probes are useful for

CC producing a microarray for predicting, measuring and displaying gene  
CC expression in samples derived from human placenta. The probes are useful  
CC for antenatal diagnosis of human genetic disorders  
XX  
SQ Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;

Query Match 75.3%; Score 12.8; DB 4; Length 80;  
Best Local Similarity 56.2%; Pred. No. 1.1e+04;  
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 CUGAUUUCAGG 17  
DB 57 CTGATTGCATTTCAGG 42

RESULT 35  
ABA40677/C  
ID ABA40677 standard; DNA; 80 BP.

XX ABA40677;  
XX  
XX 23-JAN-2002 (first entry)

DE Probe #19143 for gene expression analysis in human heart cell sample.

XX Human; gene expression; heart; microarray; vascular system; probe;  
KM cardiovascular disease; hypertension; cardiac arrhythmia;  
XX congenital heart disease; ss.

OS Homo sapiens.

XX WO200157274-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000666.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488899/53.

XX Single exon nucleic acid probes for analyzing gene expression in human  
XX hearts.

XX Claim 4; SEQ ID NO 19143; 530pp; English.

CC The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart. The  
CC present sequence is one such probe. The probes may be used for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from the human heart via microarrays. By measuring gene expression, the  
CC probes are useful for predicting, diagnosing, grading, staging,  
CC monitoring and prognosing diseases of the human heart and vascular system  
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and  
CC congenital heart disease. Note: The sequence data for this patent did not  
CC form part of the printed specification, but was obtained in electronic  
CC format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;

Query Match 75.3%; Score 12.8; DB 4; Length 80;  
Best Local Similarity 56.2%; Pred. No. 1.1e+04;  
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 CUGAUUUCAGG 17  
DB 57 CTGATTGCATTTCAGG 42

RESULT 36  
AAK50790/C  
ID AAK50790 standard; DNA; 80 BP.

XX AAK50790;

XX 06-NOV-2001 (first entry)

DE Human bone marrow expressed single exon probe SEQ ID NO: 25347.

XX Human; bone marrow expressed exon; gene expression analysis; probe;  
KM microarray; cancer; leukemia; lymphoma; myeloma; ss.

XX Homo sapiens.

XX WO200157276-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000668.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing  
XX gene expression in human bone marrow.

XX Example 4; SEQ ID NO 25347; 658bp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid  
XX probes which are derived from genomic sequences expressed in the human  
XX bone marrow. They can be used to measure gene expression in bone marrow  
XX samples, which may enable the improved diagnosis and treatment of cancers  
XX such as lymphoma, leukemia and myeloma. The present sequence is one of  
XX the probes of the invention

XX Claim 4; SEQ ID NO 25347; 658bp + Sequence Listing; English.

CC The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart. The  
CC present sequence is one such probe. The probes may be used for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from the human heart via microarrays. By measuring gene expression, the  
CC probes are useful for predicting, diagnosing, grading, staging,  
CC monitoring and prognosing diseases of the human heart and vascular system  
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and  
CC congenital heart disease. Note: The sequence data for this patent did not  
CC form part of the printed specification, but was obtained in electronic  
CC format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;

Query Match 75.3%; Score 12.8; DB 4; Length 80;  
Best Local Similarity 56.2%; Pred. No. 1.1e+04;  
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 CUGAUUUCAGG 17  
DB 57 CTGATTGCATTTCAGG 42

RESULT 37  
AAK24792/C

ID AAK24792 standard; DNA; 80 BP.

XX AAK24792;

XX 05-NOV-2001 (first entry)

XX Human brain expressed single exon probe SEQ ID NO: 24783.

XX Human; brain expressed exon; gene expression analysis; probe; microarray;  
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;  
 XX ss.  
 OS Homo sapiens.  
 PN WO200157275-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000667.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 DR WPI; 2001-483446/52.  
 XX  
 PT Single exon nucleic acid probes for analyzing gene expression in human  
 PT brains.  
 PS Example 4; SEQ ID NO 24783; 650bp + Sequence Listing; English.  
 XX  
 CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC brain. They can be used to measure gene expression in brain cell samples,  
 CC which may enable the diagnosis and improved treatment of nervous system  
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
 CC epilepsy and cancers. The present sequence is one of the probes of the  
 CC invention.  
 SQ Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;  
 QY  
 Query Match 75.3%; Score 12.8; DB 4; Length 80;  
 Best Local Similarity 56.2%; Pred. No. 1.1e+04;  
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 DB 2 CUGAUUUCAGG 17  
 57 CTGATTGCATTTCAGG 42  
 RESULT 39  
 ABS50382/C  
 ID ABS50382 standard; DNA; 80 BP.  
 AC  
 XX ABS50382;  
 XX  
 DT 25-FEB-2003 (first entry)  
 XX  
 DE Human liver single exon probe, SEQ ID No 25372.  
 XX  
 KW Human; single exon nucleic acid probe; liver; cirrhosis;  
 KW hyperlipoproteinemia; hyperlipidaemia; hypercholesterolaemia;  
 KW coronary heart disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157273-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000664.  
 XX

PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 DR WPI; 2001-48898/53.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human adult liver.  
 PS Claim 4; SEQ ID NO 25372; 658bp; English.  
 XX  
 CC The invention relates to a single exon nucleic acid probe (SENP) (1) for  
 CC measuring human gene expression in a sample derived from human adult  
 CC liver, comprising one of 1109 defined nucleotide sequences given in the  
 CC specification (or complements/ fragments). The probe hybridizes at high  
 CC stringency to a nucleic acid molecule expressed in the human adult liver.  
 CC (1) may be used for predicting, measuring and displaying gene expression  
 CC in samples derived from human adult liver. The genes identified may be  
 CC involved in genetic liver diseases such as cirrhosis,  
 CC hyperlipoproteinemia, hyperlipidaemia and hypercholesterolaemia which is  
 CC associated with coronary heart disease. ABS25011-ABS51005 represent human  
 CC liver single exon nucleic acid probes of the invention. Note: The  
 CC sequence information for this patent does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 SQ Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;  
 QY  
 Query Match 75.3%; Score 12.8; DB 4; Length 80;  
 Best Local Similarity 56.2%; Pred. No. 1.1e+04;  
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 DB 2 CUGAUUUCAGG 17  
 57 CTGATTGCATTTCAGG 42  
 RESULT 39  
 ABS24274/C  
 ID ABS24274 standard; DNA; 80 BP.  
 AC  
 XX ABS24274;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human genome-derived single exon probe ORF from lung SEQ ID No 24265.  
 XX  
 KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hereditary-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease; open reading frame; ORF.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200186003-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000665.  
 XX

04-FEB-2000; 2000US-0180312P.  
 26-MAY-2000; 2000US-0207456P.  
 30-JUN-2000; 2000US-00608408.  
 03-AUG-2000; 2000US-00632366.  
 21-SEP-2000; 2000US-0234687P.  
 27-SEP-2000; 2000US-0236359P.  
 04-OCT-2000; 2000US-00024263.  
 (MOLE-) MOLECULAR DYNAMICS INC.  
 Penn SG, Hanzel DK, Chen W, Rank DR;  
 WPI; 2002-114183/15.  
 Spatially-addressable set of single exon nucleic acid probes, used to  
 measure gene expression in human lung samples.  
 Claim 4; SEQ ID NO 24265; 634bp; English.

The invention relates to a spatially-addressable set of single exon  
 nucleic acid probes for measuring gene expression in a sample derived  
 from human lung comprising single exon nucleic acid probes having one of  
 12614 nucleic acid sequences mentioned in the specification, or their  
 complements or the 12387 open reading frames derived from the 12614  
 probes. Also included are a microarray comprising the novel set of probes  
 ; the novel set of probes which hybridize at high stringency to a nucleic  
 acid expressed in the human lung; measuring gene expression in a sample  
 derived from human lung; comprising (a) contacting the array with a  
 collection of detectably labeled nucleic acids derived from human lung  
 mRNA; and (b) measuring the label detectably bound to each probe of the  
 array; identifying exons in a eukaryotic genome, comprising (a)  
 algorithmically predicting at least one exon from genomic sequences of  
 the eukaryote; and (b) detecting specific hybridisation of detectably  
 labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 having a fragment identical to the predicted exon, the probe is included  
 in the above mentioned microarray; assigning exons to a single gene,  
 comprising (a) identifying exons from genomic sequence by the method  
 above and (b) measuring the expression of each of the exons in several  
 tissues and/or cell types using hybridisation to a single exon  
 microarrays having a probe with the exon, where a common pattern of  
 expression of the exons in the tissues and/or cell types indicates that  
 the exons should be assigned to a single gene; a peptide comprising one  
 of 12011 sequences, mentioned in the specification, or encoded by the  
 probes/open reading frames (ORF). The probes are used for gene expression  
 analysis, and for identifying exons in a gene, particularly using human  
 lung derived mRNA and for the study of lung diseases such as asthma, lung  
 cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
 disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
 tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
 Rudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
 histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
 Karsagen's syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
 dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
 present sequence is a single exon probe open reading frame of the  
 invention. Note: The sequence data for this patent did not form part of  
 the printed specification, but was obtained in electronic format directly  
 from WIP0 at ftp.wip0.int/pub/published\_pct\_sequences

Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;  
 Query Match 75.3%; Score 12.8; DB 6; Length 80;  
 Best Local Similarity 56.2%; Pred. No. 1.1e+04;  
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 Db 2 CUGAUUUCAUUGCAGG 17  
 57 CTGATGACATTTCAGG 42

RESULT 40  
 ACD81396  
 ID ACD81396 standard; DNA; 100 BP.  
 XX

ACD81396;  
 19-SEP-2003 (first entry)  
 E. coli K12 MG1655 biochip probe SEQ ID 12672.  
 Biochip; gene expression; gut; diagnostic; detection; probe; ss.  
 Escherichia coli.  
 EP1260592-A1.  
 27-NOV-2002.  
 17-MAY-2001; 2001EP-00112179.  
 17-MAY-2001; 2001EP-00112179.  
 (MMGB-) MMGB-BIOTECH AG.  
 Donner H, Drescher B, Huber A, Weber J;  
 WPI; 2003-241155/24.  
 Biochip containing probes complementary with open reading frames in  
 Escherichia coli K12, useful for detecting gene expression and expression  
 patterns.  
 Claim 3; Page 1973; 2004pp; German.

This invention describes a novel biochip comprising probe spots, each  
 containing many identical probes. The probes are nucleotide sequences of  
 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at  
 least one includes a segment of at least 20 bases identical with, or  
 complementary to, a segment of an open reading frame (orf) of Escherichia  
 coli K12. The biochip is used for specific detection of gene expression  
 in K12 and for determining the gene expression pattern, e.g. for  
 diagnostic determination of which E. coli strains are present in the gut,  
 and to determine the effects of e.g. growth media on gene expression. The  
 biochip provides a comprehensive as possible detection of the K12  
 genome, with simultaneous analysis of many different genes with a single  
 device, and comparison of gene expression between K12 and its mutants or  
 other E. coli strains in a single experiment. Apart from qualitative and  
 quantitative information about gene expression, it also allows  
 measurements of population densities for the various strains. The use of  
 synthetic oligonucleotides for preparation of probes allows free  
 variation in probe length and ensures high purity (and thus selectivity,  
 reactivity and reproducibility); also synthetic probes are generally  
 shorter than probes prepared by polymerase chain reaction. ACD86731 to  
 ACD81540 represent oligonucleotide probes used with the biochip described  
 in the invention

Sequence 100 BP; 27 A; 21 C; 30 G; 22 T; 0 U; 0 Other;  
 Query Match 75.3%; Score 12.8; DB 8; Length 100;  
 Best Local Similarity 62.5%; Pred. No. 1.1e+04;  
 Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 Db 2 CUGAUUUCAUUGCAGG 17  
 11 CTGATGACATTTCAGG 26  
 Search completed: May 13, 2005, 17:06:01  
 Job time : 131.827 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2005, 16:59:31 ; Search time 42.0364 Seconds  
(without alignments)  
661.730 Million cell updates/sec

Title: US-09-927-046-143

Perfect score: 17

Sequence: 1 ccgaaucauagcag 17

Scoring table: IDENTITY\_NUC  
Gapco 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1330268

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

Issued Patents.NA: \*  
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2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/prodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13.4	78.8	25	4	US-09-396-196G-54192
C 2	13.4	78.8	25	4	US-09-396-196G-60898
C 3	13.4	78.8	25	4	US-09-396-196G-119128
C 4	12.4	72.9	20	4	US-09-422-978-9923
C 5	12.4	72.9	25	4	US-09-396-196G-3128
C 6	12.4	72.9	25	4	US-09-396-196G-3129
C 7	12.4	72.9	25	4	US-09-396-196G-27979
C 8	12.4	72.9	25	4	US-09-396-196G-105607
C 9	12.4	72.9	31	3	US-09-230-199-17
C 10	12.4	72.9	49	3	US-09-365-121-10
C 11	12.4	72.9	49	3	US-09-365-121-11
C 12	12.4	72.9	49	4	US-09-867-193-10
C 13	12.4	72.9	49	4	US-09-867-193-11
C 14	12.4	71.8	20	3	US-08-199-219-2
C 15	12.2	71.8	25	4	US-09-189-653-9
C 16	12.2	71.8	25	4	US-09-396-196G-75597
C 17	12.2	71.8	25	4	US-09-396-196G-75598
C 18	12.2	71.8	26	3	US-09-245-041-60
C 19	12.2	71.8	26	4	US-09-358-058-61
C 20	12.2	71.8	26	4	US-09-893-238-60
C 21	12.2	71.8	30	4	US-09-426-776A-8
C 22	12.2	70.6	25	4	US-09-396-196G-108816
C 23	12.2	70.6	47	4	US-09-422-978-3740
C 24	12.2	70.6	57	4	US-09-513-999C-15276
C 25	11.8	69.4	20	3	US-09-073-567-11
C 26	11.8	69.4	20	3	US-09-073-567-34
C 27	11.8	69.4	20	3	US-09-280-805-157

28	11.8	69.4	21	2	US-08-811-492-53	Sequence 53, Appl
29	11.8	69.4	21	5	PCT-US96-10545A-53	Sequence 53, Appl
30	11.8	69.4	24	3	US-09-002-361-24	Sequence 24, Appl
31	11.8	69.4	25	2	US-08-811-492-52	Sequence 52, Appl
C 32	11.8	69.4	25	4	US-09-396-196G-22517	Sequence 22517, A
C 33	11.8	69.4	25	4	US-09-396-196G-48638	Sequence 48638, A
C 34	11.8	69.4	25	4	US-09-396-196G-88078	Sequence 88078, A
C 35	11.8	69.4	25	4	US-09-396-196G-88943	Sequence 88943, A
C 36	11.8	69.4	25	4	US-09-396-196G-89944	Sequence 89944, A
C 37	11.8	69.4	25	5	PCT-US96-10545A-52	Sequence 52, Appl
C 38	11.8	69.4	26	1	US-08-476-634-3	Sequence 3, Appl
C 39	11.8	69.4	26	1	US-08-484-518-3	Sequence 3, Appl
C 40	11.8	69.4	26	1	US-08-943-834-3	Sequence 3, Appl
C 41	11.8	69.4	51	4	US-09-443-199C-813	Sequence 813, Appl
C 42	11.8	69.4	51	4	US-09-443-199C-814	Sequence 814, Appl
C 43	11.8	69.4	65	4	US-08-956-171E-2894	Sequence 2894, Appl
C 44	11.8	69.4	65	4	US-08-781-986A-2894	Sequence 2894, Appl
C 45	11.8	69.4	68	4	US-09-313-299A-1919	Sequence 1919, Appl
C 46	11.8	69.4	84	4	US-09-513-999C-27774	Sequence 27774, A
C 47	11.8	69.4	90	4	US-09-621-976-9330	Sequence 9330, Appl
C 48	11.8	69.4	94	1	US-08-270-985-7	Sequence 7, Appl
C 49	11.8	69.4	94	3	US-08-478-208-11	Sequence 11, Appl
C 50	11.6	68.2	47	4	US-09-671-317-673	Sequence 673, Appl
C 51	11.4	67.1	19	4	US-09-696-791-263	Sequence 2693, Appl
C 52	11.4	67.1	19	4	US-09-696-791-263	Sequence 2694, Appl
C 53	11.4	67.1	22	4	US-09-548-797B-21	Sequence 21, Appl
C 54	11.4	67.1	25	4	US-09-396-196G-1653	Sequence 1653, Appl
C 55	11.4	67.1	25	4	US-09-396-196G-27978	Sequence 27978, A
C 56	11.4	67.1	25	4	US-09-396-196G-71293	Sequence 71293, A
C 57	11.4	67.1	25	4	US-09-396-196G-72224	Sequence 72224, A
C 58	11.4	67.1	25	4	US-09-396-196G-76507	Sequence 76507, A
C 59	11.4	67.1	25	4	US-09-396-196G-115075	Sequence 115075, A
C 60	11.4	67.1	25	4	US-09-396-196G-115076	Sequence 115076, A
C 61	11.4	67.1	25	4	US-09-396-196G-117033	Sequence 117033, A
C 62	11.4	67.1	25	4	US-09-396-196G-117034	Sequence 117034, A
C 63	11.4	67.1	25	4	US-09-396-196G-117035	Sequence 117035, A
C 64	11.4	67.1	25	4	US-09-396-196G-117036	Sequence 117036, A
C 65	11.4	67.1	25	4	US-09-396-196G-117037	Sequence 117037, A
C 66	11.4	67.1	25	4	US-09-396-196G-117038	Sequence 117038, A
C 67	11.4	67.1	40	1	US-08-086-428B-104	Sequence 104, Appl
C 68	11.4	67.1	40	2	US-08-468-570-104	Sequence 104, Appl
C 69	11.4	67.1	40	2	US-08-290-665A-208	Sequence 208, Appl
C 70	11.4	67.1	40	4	US-08-466-601A-104	Sequence 104, Appl
C 71	11.4	67.1	40	5	PCT-US95-10398-208	Sequence 208, Appl
C 72	11.4	67.1	73	4	US-09-513-999C-15000	Sequence 15000, A
C 73	11.4	67.1	78	3	US-09-058-483-12	Sequence 12, Appl
C 74	11.4	67.1	78	3	US-09-058-483-13	Sequence 13, Appl
C 75	11.4	67.1	78	3	US-09-058-483-14	Sequence 14, Appl
C 76	11.4	67.1	78	3	US-09-058-483-15	Sequence 15, Appl
C 77	11.4	67.1	89	4	US-09-621-976-8165	Sequence 8165, Appl
C 78	11.2	65.9	20	4	US-09-232-786-113	Sequence 113, Appl
C 79	11.2	65.9	21	4	US-09-422-978-10268	Sequence 10268, A
C 80	11.2	65.9	23	3	US-09-440-509-11	Sequence 11, Appl
C 81	11.2	65.9	24	3	US-09-153-310-30	Sequence 30, Appl
C 82	11.2	65.9	25	1	US-07-991-466-1	Sequence 1, Appl
C 83	11.2	65.9	25	1	US-08-178-660-1	Sequence 1, Appl
C 84	11.2	65.9	25	1	US-08-032-856-1	Sequence 1, Appl
C 85	11.2	65.9	25	4	US-09-396-196G-3003	Sequence 3003, Appl
C 86	11.2	65.9	25	4	US-09-396-196G-3020	Sequence 3020, Appl
C 87	11.2	65.9	25	4	US-09-396-196G-7820	Sequence 7820, Appl
C 88	11.2	65.9	25	4	US-09-396-196G-25577	Sequence 25577, A
C 89	11.2	65.9	25	4	US-09-396-196G-75547	Sequence 75547, A
C 90	11.2	65.9	25	4	US-09-396-196G-57277	Sequence 57277, A
C 91	11.2	65.9	25	4	US-09-396-196G-67393	Sequence 67393, A
C 92	11.2	65.9	25	4	US-09-396-196G-67394	Sequence 67394, A
C 93	11.2	65.9	25	4	US-09-396-196G-7303	Sequence 7303, A
C 94	11.2	65.9	25	4	US-09-396-196G-75546	Sequence 75546, A
C 95	11.2	65.9	25	4	US-09-396-196G-75547	Sequence 75547, A
C 96	11.2	65.9	25	4	US-09-396-196G-81730	Sequence 81730, A
C 97	11.2	65.9	25	4	US-09-396-196G-81748	Sequence 81748, A
C 98	11.2	65.9	25	4	US-09-396-196G-97711	Sequence 97711, A
C 99	11.2	65.9	25	4	US-09-396-196G-97712	Sequence 97712, A
C 100	11.2	65.9	25	4	US-09-396-196G-126478	Sequence 126478, A

## ALIGNMENTS

## RESULT 1

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US-09-396-196G-54192/c
; Sequence 54192, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54192
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-54192

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Query Match      78.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 53.3%; Pred. No. 6.9e+02;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

```

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QY      3 UGAUUUCAUUGCAGG 17
      : |||:|||||
DB      25 TGCTTCATTCGACGG 11

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## RESULT 2

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US-09-396-196G-60898
; Sequence 60898, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60898
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60898

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Query Match      78.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 53.3%; Pred. No. 6.9e+02;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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QY      1 CCUGAUUUCAUUGCA 15
      |||:|||||
DB      10 CCTGATTCATTGAA 24

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RESULT 3
US-09-396-196G-119128/c
; Sequence 119128, Application US/09396196G
; Patent No. 6821724

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; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119128
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-119128

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Query Match      76.5%; Score 13; DB 4; Length 25;
Best Local Similarity 53.8%; Pred. No. 1.1e+03;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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QY      3 UGAUUUCAUUGCA 15
      : |||:|||||
DB      25 TGATTCATTGCA 13

```

## RESULT 4

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US-09-422-978-9923/c
; Sequence 9923, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9923
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-8287 for SEQ 2058, in complemer
US-09-422-978-9923

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Query Match      72.9%; Score 12.4; DB 4; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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QY      1 CCUGAUUUCAUUGC 14
      |||:|||||
DB      20 CCTGATTAAATGC 7

```

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RESULT 5
US-09-396-196G-3128/c
; Sequence 3128, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack

```

APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3128  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-396-196G-3128

Query Match 72.9%; Score 12.4; DB 4; Length 25;  
Best Local Similarity 57.1%; Pred. No. 2.4e+03;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAUUCAUUGCAG 17  
DB 22 GATTTCATTGTAGG 9

RESULT 6  
US-09-396-196G-3129/C  
Sequence 3129, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Mittleman  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3129  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-396-196G-3129

Query Match 72.9%; Score 12.4; DB 4; Length 25;  
Best Local Similarity 57.1%; Pred. No. 2.4e+03;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAUUCAUUGCAG 17  
DB 16 GATTTCATTGTAGG 3

RESULT 7  
US-09-396-196G-27979  
Sequence 27979, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Mittleman  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 27979  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-396-196G-27979

Query Match 72.9%; Score 12.4; DB 4; Length 25;  
Best Local Similarity 57.1%; Pred. No. 2.4e+03;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 CUGAUUCAUUGCA 15  
DB 7 CTGATTTCATGCA 20

RESULT 8  
US-09-396-196G-105607/C  
Sequence 105607, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Mittleman  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 105607  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-396-196G-105607

Query Match 72.9%; Score 12.4; DB 4; Length 25;  
Best Local Similarity 57.1%; Pred. No. 2.4e+03;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGAUUCAUUGCAG 16  
DB 17 TGATTTCAGTCAG 4

RESULT 9  
US-09-230-199-17/C  
Sequence 17, Application US/09230199  
Patent No. 6294378  
GENERAL INFORMATION:  
APPLICANT: Houghton, Alan  
APPLICANT: Bartido, Shirley M.  
APPLICANT: Xu, Yigang  
APPLICANT: Wang, Siqun  
TITLE OF INVENTION: Method and Reagents for Genetic  
TITLE OF INVENTION: Immunization  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Oppehl & Larson  
STREET: PO Box 5270  
CITY: Frisco  
STATE: CO  
COUNTRY: USA  
ZIP: 80443-5270  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: US/09/230,199
/ FILING DATE:
/ CLASSIFICATION:
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US97/12675
/ FILING DATE: 18-JUL-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Marina T. Larson
/ REGISTRATION NUMBER: 32,038
/ REFERENCE/DOCKET NUMBER: MSK-P-012
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (970) 668-2050
/ TELEFAX: (970) 668-2082
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 31
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: genomic DNA
/ HYPOTHETICAL: no
/ ANTI-SENSE: no
US-09-230-199-17
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Query Match 72.9%; Score 12.4; DB 3; Length 49;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 CCGAUUUCAUUGC 14
Db 24 CCTGATTCAGTCG 11
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RESULT 10
US-09-365-121-10/c
/ Sequence 10, Application US/09365121
/ Patent No. 6297365
/ GENERAL INFORMATION:
/ APPLICANT: ADAMS, Christopher C.
/ APPLICANT: BRENTANO, Steven T.
/ APPLICANT: SCHROTH, Gary P.
/ TITLE OF INVENTION: DECOY PROBES
/ FILE REFERENCE: US Seq. Listing
/ CURRENT APPLICATION NUMBER: US/09/365,121
/ CURRENT FILING DATE: 1999-07-30
/ EARLIER APPLICATION NUMBER: 60/094,979
/ EARLIER FILING DATE: 1998-07-31
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 10
/ LENGTH: 49
/ TYPE: DNA
/ ORGANISM: synthetic construct
US-09-365-121-10
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```
Query Match 72.9%; Score 12.4; DB 3; Length 49;
Best Local Similarity 57.1%; Pred. No. 2.7e+03;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 3 UGAUUCUUAUUGCAG 16
Db 25 TGATTTCAGTCGAG 12
```

```
RESULT 11
US-09-365-121-11/c
/ Sequence 11, Application US/09365121
/ Patent No. 6297365
/ GENERAL INFORMATION:
/ APPLICANT: ADAMS, Christopher C.
/ APPLICANT: BRENTANO, Steven T.
/ APPLICANT: SCHROTH, Gary P.
```

```
/ TITLE OF INVENTION: DECOY PROBES
/ FILE REFERENCE: US Seq. Listing
/ CURRENT APPLICATION NUMBER: US/09/365,121
/ CURRENT FILING DATE: 1999-07-30
/ EARLIER APPLICATION NUMBER: 60/094,979
/ EARLIER FILING DATE: 1998-07-31
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 11
/ LENGTH: 49
/ TYPE: DNA
/ ORGANISM: synthetic construct
US-09-365-121-11
```

```
Query Match 72.9%; Score 12.4; DB 3; Length 49;
Best Local Similarity 57.1%; Pred. No. 2.7e+03;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 3 UGAUUCUUAUUGCAG 16
Db 25 TGATTTCAGTCGAG 12
```

```
RESULT 12
US-09-867-193-10/c
/ Sequence 10, Application US/09867193
/ Patent No. 6602668
/ GENERAL INFORMATION:
/ APPLICANT: ADAMS, Christopher C.
/ APPLICANT: BRENTANO, Steven T.
/ APPLICANT: SCHROTH, Gary P.
/ TITLE OF INVENTION: DECOY PROBES
/ FILE REFERENCE: US Seq. Listing
/ CURRENT APPLICATION NUMBER: US/09/867,193
/ CURRENT FILING DATE: 2001-05-29
/ PRIOR APPLICATION NUMBER: 09/365,121
/ PRIOR FILING DATE: 1999-07-30
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 10
/ LENGTH: 49
/ TYPE: DNA
/ ORGANISM: synthetic construct
US-09-867-193-10
```

```
Query Match 72.9%; Score 12.4; DB 4; Length 49;
Best Local Similarity 57.1%; Pred. No. 2.7e+03;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 3 UGAUUCUUAUUGCAG 16
Db 25 TGATTTCAGTCGAG 12
```

```
RESULT 13
US-09-867-193-11/c
/ Sequence 11, Application US/09867193
/ Patent No. 6602668
/ GENERAL INFORMATION:
/ APPLICANT: ADAMS, Christopher C.
/ APPLICANT: BRENTANO, Steven T.
/ APPLICANT: SCHROTH, Gary P.
/ TITLE OF INVENTION: DECOY PROBES
/ FILE REFERENCE: US Seq. Listing
/ CURRENT APPLICATION NUMBER: US/09/867,193
/ CURRENT FILING DATE: 2001-05-29
/ PRIOR APPLICATION NUMBER: 09/365,121
/ PRIOR FILING DATE: 1999-07-30
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 11
/ LENGTH: 49
/ TYPE: DNA
```

ORGANISM: sythetic construct  
US-09-867-193-11

Query Match  
Best Local Similarity 72.9%; Score 12.4; DB 4; Length 49;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGAUUUCAGUCAG 16  
DB 25 TGATTTCAGTGCAG 12

RESULT 14  
US-08-199-219-2  
Sequence 2, Application US/08199219

Patent No. 6031151  
Patent No. 6031151 5698768  
GENERAL INFORMATION:  
APPLICANT: DRAPER, JOHN  
TITLE OF INVENTION: CALUS-SPECIFIC PROMOTERS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:

ADDRESSEE: HALE AND DORR  
STREET: 1455 PENNSYLVANIA AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/199,219  
FILING DATE: 01 MARCH 1994  
PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/GB92/01602  
PRIOR APPLICATION DATA: FILING DATE: 02 SEPTEMBER 1992

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:

NAME/KEY: misc.feature  
LOCATION: 1..20  
OTHER INFORMATION: /product= "IPCR 1 PRIMER"

US-08-199-219-2

Query Match  
Best Local Similarity 71.8%; Score 12.2; DB 3; Length 20;  
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAGUCAG 17  
DB 2 CCTGACTTATTCGCCG 18

RESULT 15  
US-09-189-653-9  
Sequence 9, Application US/09189653

Patent No. 6171792  
GENERAL INFORMATION:  
APPLICANT: Brent, Roger  
APPLICANT: Xu, C. Wilson  
APPLICANT: Mendelsohn, Andrew R.  
APPLICANT: Lok, Walter L.

TITLE OF INVENTION: DETECTION SYSTEMS FOR REGISTERING  
FILE REFERENCE: 00786/317002

CURRENT APPLICATION NUMBER: US/09/189,653

CURRENT FILING DATE: 1998-11-10  
EARLIER APPLICATION NUMBER: 60/065,273  
EARLIER FILING DATE: 1997-11-10  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 9  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-189-653-9

QY 1 CCUGAUUUCAGUCAG 17  
DB 2 CCTGACTTATTCGCCG 18

Query Match  
Best Local Similarity 71.8%; Score 12.2; DB 3; Length 25;  
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

RESULT 16  
US-09-396-196G-75597/C  
Sequence 75597, Application US/09396196G

Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Mittleman  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 75597  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-75597

QY 1 CCUGAUUUCAGUCAG 17  
DB 23 CCTGACTTATTCGCCG 7

Query Match  
Best Local Similarity 71.8%; Score 12.2; DB 4; Length 25;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

RESULT 17  
US-09-396-196G-75598/C  
Sequence 75598, Application US/09396196G

Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Mittleman  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 75598  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus

QY 1 CCUGAUUUCAGUCAG 17  
DB 23 CCTGACTTATTCGCCG 7

US-09-396-196G-75598

Query Match 71.8%; Score 12.2; DB 4; Length 25;  
Best Local Similarity 58.8%; Pred. No. 3.1e+03;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAUUGCAGG 17

DB 17 CCTGATGACTTGACAGG 1

RESULT 18

US-09-245-041-60/c  
; Sequence 60, Application US/09245041  
; Patent No. 6274339  
; GENERAL INFORMATION:  
; APPLICANT: Moore, K.  
; APPLICANT: Nagle, D.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT  
; TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY  
; FILE REFERENCE: 7853-136  
; CURRENT APPLICATION NUMBER: US/09/245,041  
; EARLIER FILING DATE: 1999-02-05  
; EARLIER APPLICATION NUMBER: 60/093,630  
; EARLIER FILING DATE: 1998-07-21  
; EARLIER APPLICATION NUMBER: 60/104,978  
; EARLIER FILING DATE: 1998-10-20  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 60  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
US-09-245-041-60

Query Match 71.8%; Score 12.2; DB 3; Length 26;  
Best Local Similarity 52.9%; Pred. No. 3.1e+03;  
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAUUGCAGG 17

DB 21 CCTGATGACTTGACAGG 5

RESULT 19

US-09-358-055B-61/c  
; Sequence 61, Application US/09358055B  
; Patent No. 6713277  
; GENERAL INFORMATION:  
; APPLICANT: Moore, K.  
; APPLICANT: Nagle, D.L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND  
; TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS INCLUDING  
; TITLE OF INVENTION: OBESITY  
; FILE REFERENCE: 7853-151  
; CURRENT APPLICATION NUMBER: US/09/358,055B  
; CURRENT FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: 09/245,041  
; PRIOR FILING DATE: 1999-02-05  
; NUMBER OF SEQ ID NOS: 153  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 61  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-358-055B-61

Query Match 71.8%; Score 12.2; DB 4; Length 26;  
Best Local Similarity 52.9%; Pred. No. 3.1e+03;  
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAUUGCAGG 17  
DB 21 CCTGATGACTTGACAGG 5

RESULT 20

US-09-893-238-60/c  
; Sequence 60, Application US/09893238  
; Patent No. 6727348  
; GENERAL INFORMATION:  
; APPLICANT: Moore, K.  
; APPLICANT: Nagle, D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND  
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY  
; FILE REFERENCE: 7853-237  
; CURRENT APPLICATION NUMBER: US/09/893,238  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: 09/245,041  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: 60/093,630  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: 60/104,978  
; PRIOR FILING DATE: 1998-10-20  
; NUMBER OF SEQ ID NOS: 129  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 60  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-893-238-60

Query Match 71.8%; Score 12.2; DB 4; Length 26;  
Best Local Similarity 52.9%; Pred. No. 3.1e+03;  
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAUUGCAGG 17

DB 21 CCTGATGACTTGACAGG 5

RESULT 21

US-09-426-776A-8  
; Sequence 8, Application US/09426776A  
; Patent No. 6733997  
; GENERAL INFORMATION:  
; APPLICANT: DING, Jeak Ling  
; APPLICANT: TAN, Ngan Soon  
; APPLICANT: HO, Bow  
; APPLICANT: LAM, Toong Jin  
; TITLE OF INVENTION: ISOLATED NUCLEIC ACIDS ENCODING A SECRETORY SIGNAL FOR EXPRESSION  
; TITLE OF INVENTION: SECRETION OF HETEROLOGOUS RECOMBINANT PROTEINS  
; FILE REFERENCE: 1781-0178P  
; CURRENT APPLICATION NUMBER: US/09/426,776A  
; CURRENT FILING DATE: 1999-10-26  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Bamgal forward primer with BamHI restriction site and some beta-galactosidase sequence derived from bacteria  
US-09-426-776A-8

Query Match 71.8%; Score 12.2; DB 4; Length 30;  
Best Local Similarity 47.1%; Pred. No. 3.2e+03;  
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAUUGCAGG 17

DB 21 CCTGATGACTTGACAGG 5

Db 11 CGTATTCGTTGCCG 27

## RESULT 22

US-09-396-196G-108816/C  
; Sequence 108816, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittlemann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 108816  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-108816

Query Match 70.6%; Score 12; DB 4; Length 25;

Best Local Similarity 58.3%; Pred. No. 4e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 6 UUCAUUGCAGG 17

Db 16 TTTCATTCGACG 5

## RESULT 23

US-09-422-978-3740/C  
; Sequence 3740, Application US/09422978  
; Patent No. 6537751  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumentfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.020CPI  
; CURRENT APPLICATION NUMBER: US/09/422,978  
; CURRENT FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: US 09/298,850  
; EARLIER FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 60/109,732  
; EARLIER FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: US 60/082,614  
; EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 3740  
; LENGTH: 47  
; TYPE: DNA  
; ORGANISM: Homo Sapiens

FEATURE:  
NAME/KEY: allele  
LOCATION: 24

OTHER INFORMATION: 99-10307-115 : polymorphic base A or G  
US-09-422-978-3740

Query Match 70.6%; Score 12; DB 4; Length 47;

Best Local Similarity 50.0%; Pred. No. 4.4e+03; Mismatches 1; Indels 0; Gaps 0;

Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 3 UCAUUUCAUUGCAG 16

Db 24 YGATTTCTTTGCG 11

## RESULT 24

US-09-513-999C-15276  
; Sequence 15276, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59,US2,REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 15276  
; LENGTH: 57  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-513-999C-15276

Query Match 70.6%; Score 12; DB 4; Length 57;

Best Local Similarity 58.3%; Pred. No. 4.6e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 6 UUCAUUGCAGG 17

Db 4 TTTCATTCGACG 15

## RESULT 25

US-09-073-567-11/C  
; Sequence 11, Application US/09073567  
; Patent No. 6013786  
; GENERAL INFORMATION:  
; APPLICANT: Jiaodong Chen  
; APPLICANT: Sudhir Agrawal  
; APPLICANT: Ruimen Zhang  
; TITLE OF INVENTION: MDM2-SPECIFIC ANTISENSE OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive, 32nd Floor  
CITY: Chicago  
STATE: IL  
COUNTRY: United States of America  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/073,567  
FILING DATE:

## CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Greenfield, Michael S.  
REGISTRATION NUMBER: 37,147  
REFERENCE/DOCKET NUMBER: 98,057-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 913-0001  
TELEFAX: (312) 913-0002

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: nucleic acid

HYPOTHETICAL: NO

ANTI-SENSE: NO  
US-09-073-567-11

Query Match 69.4%; Score 11.8; DB 3; Length 20;  
Best Local Similarity 46.7%; Pred. No. 4.9e+03;  
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 3 UGAUUCUAGCAGG 17  
DB 16 TCATTTCATTCATG 2

## RESULT 26

US-09-073-567-34  
Sequence 34, Application US/09073567  
Patent No. 6013786  
GENERAL INFORMATION:  
APPLICANT: Jiahdong Chen  
APPLICANT: Sudhir Agrawal  
APPLICANT: Ruiwen Zhang  
TITLE OF INVENTION: MDM2-SPECIFIC ANTISENSE OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive, 32nd Floor  
CITY: Chicago  
STATE: IL  
COUNTRY: United States of America  
ZIP: 60606

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/073,567  
FILING DATE:

## CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Greenfield, Michael S.  
REGISTRATION NUMBER: 37,147  
REFERENCE/DOCKET NUMBER: 98,057-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 913-0001  
TELEFAX: (312) 913-0002  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: nucleic acid  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-09-073-567-34

Query Match 69.4%; Score 11.8; DB 3; Length 20;  
Best Local Similarity 46.7%; Pred. No. 4.9e+03;  
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 3 UGAUUCUAGCAGG 17  
DB 5 TCATTTCATTCATG 19

## RESULT 27

US-09-280-805-157  
Sequence 157, Application US/09280805  
Patent No. 6184212  
GENERAL INFORMATION:  
APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.  
APPLICANT: Graham, Brett P. Monia  
TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2

TITLE OF INVENTION: EXPRESSION  
NUMBER OF SEQUENCES: 271  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Jane Massey Licata  
STREET: 66 East Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: U.S.A.

## COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PC

OPERATING SYSTEM: WINDOWS 95

SOFTWARE: WORDPERFECT 6.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/280,805  
FILING DATE: herewith

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/048,810  
FILING DATE: March 26, 1998

ATTORNEY/AGENT INFORMATION:  
NAME: Licata, Jane Massey

REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0346

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-810-1515  
TELEFAX: 609-810-1454

INFORMATION FOR SEQ ID NO: 157:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: linear

ANTI-SENSE: Yes

US-09-280-805-157

Query Match 69.4%; Score 11.8; DB 3; Length 20;  
Best Local Similarity 46.7%; Pred. No. 4.9e+03;  
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 3 UGAUUCUAGCAGG 17  
DB 1 TCATTTCATTCATG 15

## RESULT 28

US-08-811-492-53  
Sequence 53, Application US/08811492  
Patent No. 5834247  
GENERAL INFORMATION:  
APPLICANT: COMB, DONALD G.  
APPLICANT: PERLER, FRANCINE B.  
APPLICANT: JACK, WILLIAM B.

APPLICANT: XU, MING-QUN  
APPLICANT: HODGES, ROBERT A.

APPLICANT: NOREN, CHRISTOPHER J.  
APPLICANT: CHONG, SHAORONG S.C.

APPLICANT: ADAM, ERIC  
APPLICANT: SOUTHWORTH, MAURICE

TITLE OF INVENTION: MODIFIED PROTEINS, METHODS OF THEIR  
TITLE OF INVENTION: PRODUCTION AND METHODS FOR PURIFICATION OF TARGET  
NUMBER OF SEQUENCES: 155  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.  
STREET: 32 TOZER ROAD  
CITY: BEVERLY  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 01915

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC\DOS\MS\ DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,492
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/580,555
FILING DATE: 29-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,247
FILING DATE: 28-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/146,885
FILING DATE: 03-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/004,139
FILING DATE: 09-DEC-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-036C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-927-5054
TELEFAX: 509-927-1705
TELEX:
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-811-492-53

Query Match
Best Local Similarity 69.4%; Score 11.8; DB 2; Length 21;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAGUGCA 15
DB 1 CCTGAATTCAGTCA 15

RESULT 29
PCT-US96-10545A-53
Sequence 53, Application PC/TUS9610545A
GENERAL INFORMATION:
APPLICANT: COMB, DONALD G.
APPLICANT: PERLER, FRANTINE B.
APPLICANT: JACK, WILLIAM E.
APPLICANT: XU, MING-QUN
APPLICANT: HODGES, ROBERT A.
APPLICANT: NOREN, CHRISTOPHER J.
TITLE OF INVENTION: MODIFIED PROTEINS AND METHODS OF THEIR
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
STREET: 32 TOZER ROAD
CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10545A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/580,555
FILING DATE: 29-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,247
FILING DATE: 28-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/146,885
FILING DATE: 03-NOV-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/004,139
FILING DATE: 09-DEC-1992
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-036C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
TELEX:
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US96-10545A-53

Query Match
Best Local Similarity 69.4%; Score 11.8; DB 5; Length 21;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAGUGCA 15
DB 1 CCTGAATTCAGTCA 15

RESULT 30
US-09-002-361-24
Sequence 24, Application US/09002361
Patent No. 6329516
GENERAL INFORMATION:
APPLICANT: Halling, Blak
TITLE OF INVENTION: Lepidopteran GABA-gated chloride
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,361
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ATTORNEY/AGENT INFORMATION:  
NAME: Bloom, Allen  
REGISTRATION NUMBER: 29,135  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-520-3214  
TELEFAX: 609-520-3259  
TELEX:  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-002-361-24

Query Match 69.4%; Score 11.8; DB 3; Length 24;  
Best Local Similarity 53.3%; Pred. No. 5e+03;  
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 3 UGAUUUCAUUCGAG 17  
Db 5 TGAATTCATTCGCTGG 19

RESULT 31  
US-08-811-492-52/c  
Sequence 52, Application US/08811492  
Patent No. 5834247  
GENERAL INFORMATION:  
APPLICANT: COMB, DONALD G.  
APPLICANT: PERLER, FRANCINE B.  
APPLICANT: JACK, WILLIAM E.  
APPLICANT: XU, MING-QUN  
APPLICANT: HODGES, ROBERT A.  
APPLICANT: NOREN, CHRISTOPHER J.  
APPLICANT: CHONG, SHARONG S.C.  
APPLICANT: ADAM, ERIC  
APPLICANT: SOUTHWORTH, MAURICE  
TITLE OF INVENTION: MODIFIED PROTEINS, METHODS OF THEIR  
TITLE OF INVENTION: PRODUCTION AND METHODS FOR PURIFICATION OF TARGET  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 155  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.  
STREET: 32 TOZER ROAD  
CITY: BEVERLY  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 01915  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC\ DOS/MS\ DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/811,492  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/580,555  
FILING DATE: 29-DEC-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/496,247  
FILING DATE: 28-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/146,885  
FILING DATE: 03-NOV-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/004,139

FILING DATE: 09-DEC-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams, Gregory D  
REGISTRATION NUMBER: 30901  
REFERENCE/DOCKET NUMBER: NEB-036C4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 508-927-5054  
TELEFAX: 509-927-1705  
TELEX:  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-811-492-52

Query Match 69.4%; Score 11.8; DB 2; Length 25;  
Best Local Similarity 60.0%; Pred. No. 5.1e+03;  
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCUGAUUUCAUUGCA 15  
Db 25 CCGTAATTCAGTCA 11

RESULT 32  
US-09-396-196G-22517/c  
Sequence 22517, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 22517  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-396-196G-22517

Query Match 69.4%; Score 11.8; DB 4; Length 25;  
Best Local Similarity 60.0%; Pred. No. 5.1e+03;  
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 UGAUUUCAUUCGAG 17  
Db 20 TGATTCAGTCGACG 6

RESULT 33  
US-09-396-196G-49638  
Sequence 49638, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678



CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/496,247  
FILING DATE: 28-JUN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/146,885  
FILING DATE: 03-NOV-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/004,139  
FILING DATE: 09-DEC-1992  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAMS, GREGORY D.  
REGISTRATION NUMBER: 30901  
REFERENCE/DOCKET NUMBER: NEB-036C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (508) 927-5054  
TELEFAX: (508) 927-1705  
TELEX:  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US96-10545A-52

Query Match 69.4%; Score 11.8; DB 5; Length 25;  
Best Local Similarity 60.0%; Pred. No. 5.1e+03;  
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCUGAUUUCAGUGCA 15  
Db 25 CCGAATTCAGTCA 11

RESULT 38  
US-08-476-634-3/c  
Sequence 3, Application US/08476634  
Patent No. 5674995  
GENERAL INFORMATION:  
APPLICANT: Becherer, Kathleen Ann  
APPLICANT: Dattagupta, Nanibhushan  
APPLICANT: Naidu, Yathi M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: CYTOKINE SIGNAL TRANSDUCER gp130 mRNA AS INHIBITORS OF DISEASE  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Gen-Probe Incorporated  
STREET: 9880 Campus Point Drive  
CITY: San Diego  
STATE: CA  
COUNTRY: USA  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,634  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fisher, Carlos A.  
REGISTRATION NUMBER: 36,510  
REFERENCE/DOCKET NUMBER: CB1006  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-535-2807  
TELEFAX: 619-546-7929  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-476-634-3

Query Match 69.4%; Score 11.8; DB 1; Length 26;  
Best Local Similarity 53.3%; Pred. No. 5.1e+03;  
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CUGAUUUCAGUGCAG 16  
Db 22 CTAATTCAGTCA 8

RESULT 39  
US-08-484-518-3/c  
Sequence 3, Application US/08484518  
Patent No. 5747470  
GENERAL INFORMATION:  
APPLICANT: Becherer, Kathleen  
APPLICANT: Dattagupta, Nanibhushan  
APPLICANT: Naidu, Yathi M.  
TITLE OF INVENTION: METHOD FOR INHIBITING CELLULAR  
TITLE OF INVENTION: POLYMERIZATION USING ANTISENSE OLIGONUCLEOTIDES TO gp130 mRNA  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Gen-Probe Incorporated  
STREET: 9880 Campus Point Drive  
CITY: San Diego  
STATE: CA  
COUNTRY: USA  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,518  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fisher, Carlos A.  
REGISTRATION NUMBER: 36,510  
REFERENCE/DOCKET NUMBER: CB1007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-535-2807  
TELEFAX: 619-546-7929  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-484-518-3

Query Match 69.4%; Score 11.8; DB 1; Length 26;  
Best Local Similarity 53.3%; Pred. No. 5.1e+03;  
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CUGAUUUCAGUGCAG 16  
Db 22 CTAATTCAGTCA 8

## RESULT 40

US-08-943-834-3/c

; Sequence 3, Application US/08943834

; Patent No. 5780612

; GENERAL INFORMATION:

; APPLICANT: Becherer, Kathleen Ann

; APPLICANT: Dattagupta, Nanibhusan

; APPLICANT: Naidu, Yathi M.

; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR

; TITLE OF INVENTION: CYTOKINE SIGNAL TRANSDUCER SP130 mRNA AS INHIBITORS OF

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Gen-Probe Incorporated

; STREET: 9880 Campus Point Drive

; CITY: San Diego

; STATE: CA

; COUNTRY: USA

; ZIP: 92121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/943,834

; FILING DATE:

; CLASSIFICATION: 514

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/476,634

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Fisher, Carlos A.

; REGISTRATION NUMBER: 36,510

; REFERENCE/DOCKET NUMBER: CB1006

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-535-2807

; TELEFAX: 619-546-7929

; TELEX:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-943-834-3

Query Match 69.4%; Score 11.8; DB 1; Length 26;

Best Local Similarity 53.3%; Pred. No. 5.1e+03;

Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CUGAUUUCAUUGCAG 16

DB 22 CTAATTCTACTGCAG 8

Search completed: May 13, 2005, 18:27:23  
J00 time : 45.0364 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using bw model

Run on: May 13, 2005, 16:54:55 / Search time 144.964 Seconds  
(without alignments)  
717.723 Million cell updates/sec

Title: US-09-927-046-143

Perfect score: 17

Sequence: 1 ccugaaucaugcagcag 17

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 5662332 seqs, 3060109652 residues

Total number of hits satisfying chosen parameters: 5530346

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database:

Published Applications NA.\*  
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3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*  
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10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
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13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*  
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18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	16	94.1	17	10	US-09-927-046-705
4	15	88.2	15	10	US-09-927-046-5413
5	15	88.2	15	10	US-09-927-046-5414
6	15	88.2	15	10	US-09-927-046-5415
7	15	88.2	17	10	US-09-927-046-141
8	15	88.2	88	9	US-09-864-761-32170
9	14.4	84.7	25	19	US-10-719-900-534802
10	14	82.4	15	10	US-09-927-046-5412
11	14	82.4	17	10	US-09-927-046-144

C 12	14	82.4	19	19	US-10-481-613-159	Sequence 159, App
C 13	14	81.2	25	19	US-10-719-900-922893	Sequence 922893,
C 14	13.8	81.2	25	19	US-10-719-900-716006	Sequence 716006,
C 15	13.4	78.8	22	14	US-10-004-2198-12	Sequence 12, Appl
C 16	13.4	78.8	22	18	US-10-787-845-12	Sequence 12, Appl
C 17	13.4	78.8	25	19	US-10-719-900-94994	Sequence 94994, A
C 18	13.4	78.8	25	19	US-10-719-900-166732	Sequence 166732,
C 19	13.4	78.8	25	19	US-10-719-900-220262	Sequence 220262,
C 20	13.4	78.8	25	19	US-10-719-900-912524	Sequence 912524,
C 21	13.4	78.8	25	19	US-10-809-189-54192	Sequence 54192, A
C 22	13.4	78.8	25	19	US-10-809-189-60898	Sequence 60898, A
C 23	13.4	78.8	52	17	US-10-445-789-17	Sequence 17, Appl
C 24	13	76.5	15	10	US-09-927-046-5416	Sequence 5416, Ap
C 25	13	76.5	17	10	US-10-839-668-70	Sequence 70, Appl
C 26	13	76.5	17	10	US-09-927-046-1247	Sequence 1247, Ap
C 27	13	76.5	17	10	US-09-927-046-1671	Sequence 1671, Ap
C 28	13	76.5	25	19	US-10-719-900-36009	Sequence 36009,
C 29	13	76.5	25	19	US-10-719-900-491812	Sequence 491812,
C 30	13	76.5	25	19	US-10-719-900-813289	Sequence 813289,
C 31	13	76.5	25	19	US-10-809-189-119128	Sequence 119128,
C 32	13	76.5	43	19	US-10-741-849-1206	Sequence 1206, Ap
C 33	13	76.5	60	10	US-09-908-975-18678	Sequence 18678, A
C 34	12.8	75.3	21	18	US-10-751-736-12517	Sequence 12517, A
C 35	12.8	75.3	21	18	US-10-751-736-12518	Sequence 12518, A
C 36	12.8	75.3	25	19	US-10-098-263B-108838	Sequence 108838,
C 37	12.8	75.3	25	19	US-10-719-900-134100	Sequence 134100,
C 38	12.8	75.3	25	19	US-10-719-900-200558	Sequence 200558,
C 39	12.8	75.3	25	19	US-10-719-900-220971	Sequence 220971,
C 40	12.8	75.3	25	19	US-10-719-900-220972	Sequence 220972,
C 41	12.8	75.3	25	19	US-10-719-900-305150	Sequence 305150,
C 42	12.8	75.3	25	19	US-10-719-900-397006	Sequence 397006,
C 43	12.8	75.3	25	19	US-10-719-900-449435	Sequence 449435,
C 44	12.8	75.3	25	19	US-10-719-900-534803	Sequence 534803,
C 45	12.8	75.3	25	19	US-10-719-900-551683	Sequence 551683,
C 46	12.8	75.3	25	19	US-10-719-900-551813	Sequence 551813,
C 47	12.8	75.3	25	19	US-10-719-900-768159	Sequence 768159,
C 48	12.8	75.3	25	19	US-10-719-900-935189	Sequence 935189,
C 49	12.8	75.3	31	17	US-10-138-674-19717	Sequence 19717, A
C 50	12.8	75.3	31	18	US-10-287-949A-19717	Sequence 19717, A
C 51	12.8	75.3	31	18	US-10-712-633-5514	Sequence 5514, Ap
C 52	12.8	75.3	32	10	US-09-884-465A-173	Sequence 173, App
C 53	12.8	75.3	70	13	US-10-027-632-177723	Sequence 177723,
C 54	12.8	75.3	70	13	US-10-027-632-177740	Sequence 177740,
C 55	12.8	75.3	70	13	US-10-027-632-177757	Sequence 177757,
C 56	12.8	75.3	70	13	US-10-027-632-177774	Sequence 177774,
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C 59	12.8	75.3	70	17	US-10-027-632-177757	Sequence 177757,
C 60	12.8	75.3	70	17	US-10-027-632-177774	Sequence 177774,
C 61	12.8	75.3	80	9	US-09-864-761-25997	Sequence 25997, A
C 62	12.4	72.9	20	17	US-10-349-143-9923	Sequence 9923, A
C 63	12.4	72.9	25	18	US-10-483-417-4	Sequence 4, Appl
C 64	12.4	72.9	25	19	US-10-719-900-171642	Sequence 171642,
C 65	12.4	72.9	25	19	US-10-719-900-318909	Sequence 318909,
C 66	12.4	72.9	25	19	US-10-719-900-388452	Sequence 388452,
C 67	12.4	72.9	25	19	US-10-719-900-501248	Sequence 501248,
C 68	12.4	72.9	25	19	US-10-719-900-511178	Sequence 511178,
C 69	12.4	72.9	25	19	US-10-719-900-676587	Sequence 676587,
C 70	12.4	72.9	25	19	US-10-719-900-717855	Sequence 717855,
C 71	12.4	72.9	25	19	US-10-719-900-822629	Sequence 822629,
C 72	12.4	72.9	25	19	US-10-719-900-922894	Sequence 922894,
C 73	12.4	72.9	25	19	US-10-616-309-2	Sequence 2, Appl
C 74	12.4	72.9	25	19	US-10-809-189-3128	Sequence 3128, Ap
C 75	12.4	72.9	25	19	US-10-809-189-3129	Sequence 3129, Ap
C 76	12.4	72.9	25	19	US-10-809-189-27979	Sequence 27979, A
C 77	12.4	72.9	25	19	US-10-809-189-105607	Sequence 105607,
C 78	12.4	72.9	31	9	US-09-898-541-17	Sequence 17, Appl
C 79	12.4	72.9	49	9	US-09-867-193-10	Sequence 10, Appl
C 80	12.4	72.9	49	9	US-09-867-193-11	Sequence 11, Appl
C 81	12.4	72.9	49	16	US-10-375-623-10	Sequence 10, Appl
C 82	12.4	72.9	49	16	US-10-375-623-11	Sequence 11, Appl
C 83	12.4	72.9	60	10	US-09-908-975-7956	Sequence 7956, Ap
C 84	12.4	72.9	60	10	US-09-908-975-15199	Sequence 15199, A

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c 85 12.4 72.9 60 10 US-09-908-975-18798 Sequence 18798, A
c 86 12.4 72.9 65 15 US-09-908-975-30947 Sequence 30947, A
c 87 12.4 72.9 96 10 US-10-199-957A-52 Sequence 52, Appl
c 88 12.2 71.8 23 10 US-09-998-027-69 Sequence 69, Appl
c 89 12.2 71.8 23 16 US-10-165-099-69 Sequence 69, Appl
c 90 12.2 71.8 24 17 US-10-357-321-18 Sequence 18, Appl
c 91 12.2 71.8 25 9 US-09-757-309-9 Sequence 9, Appl
c 92 12.2 71.8 25 19 US-10-719-900-110582 Sequence 110582,
c 93 12.2 71.8 25 19 US-10-719-900-135687 Sequence 135687,
c 94 12.2 71.8 25 19 US-10-719-900-211703 Sequence 211703,
c 95 12.2 71.8 25 19 US-10-719-900-213920 Sequence 213920,
c 96 12.2 71.8 25 19 US-10-719-900-242369 Sequence 242369,
c 97 12.2 71.8 25 19 US-10-719-900-259682 Sequence 259682,
c 98 12.2 71.8 25 19 US-10-719-900-301695 Sequence 301695,
c 99 12.2 71.8 25 19 US-10-719-900-319494 Sequence 319494,
c 100 12.2 71.8 25 19 US-10-719-900-357532 Sequence 357532,

```

## ALIGNMENTS

```

RESULT 1
US-09-927-046-143
; Sequence 143, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloro
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-143

Query Match          100.0%; Score 17; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCUGAUUUCAUUGCAGG 17
DB      1 CCUGAUUUCAUUGCAGG 17

RESULT 2
US-09-927-046-142
; Sequence 142, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloro
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 142
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-142

Query Match          100.0%; Score 17; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCUGAUUUCAUUGCAGG 17
DB      1 CCUGAUUUCAUUGCAGG 17

RESULT 3
US-09-927-046-705
; Sequence 705, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloro
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 705
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-705

Query Match          94.1%; Score 16; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CCUGAUUUCAUUGCAGG 16
DB      2 CCUGAUUUCAUUGCAGG 17

RESULT 4
US-09-927-046-5413
; Sequence 5413, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloro
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5413
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
US-09-927-046-5413

Query Match          94.1%; Score 16; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CCUGAUUUCAUUGCAGG 17
DB      1 CCUGAUUUCAUUGCAGG 16

```

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-927-046-5413

Query Match 88.2%; Score 15; DB 10; Length 15;  
Best Local Similarity 60.0%; Pred. No. 4.4e+02;  
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUAGUUUCAGGCA 15  
|||::|::|::|::|  
DB 1 CCGATTTCATTGCA 15

RESULT 5  
US-09-927-046-5414

Sequence 5414, Application US/09927046  
Publication No. US20030064946A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc

APPLICANT: MCSwigen, Jim

APPLICANT: Thompson, Jim

APPLICANT: McKenzie, Tim

APPLICANT: Ayers, Dave

APPLICANT: Grupe, Andrew

APPLICANT: Szymowski, Edmund

TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloro

FILE REFERENCE: 249/021

CURRENT APPLICATION NUMBER: US/09/927,046

CURRENT FILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 5450

SOFTWARE: Patentin version 3.0

SEQ ID NO 5414

LENGTH: 15

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-927-046-5414

Query Match 88.2%; Score 15; DB 10; Length 15;  
Best Local Similarity 60.0%; Pred. No. 4.4e+02;  
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 CUGAUUUCAGGCA 16  
|::|::|::|::|  
DB 1 CTGATTTCATTGCG 15

RESULT 6  
US-09-927-046-5415

Sequence 5415, Application US/09927046  
Publication No. US20030064946A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc

APPLICANT: MCSwigen, Jim

APPLICANT: Thompson, Jim

APPLICANT: McKenzie, Tim

APPLICANT: Ayers, Dave

APPLICANT: Grupe, Andrew

APPLICANT: Szymowski, Edmund

TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloro

FILE REFERENCE: 249/021

CURRENT APPLICATION NUMBER: US/09/927,046

CURRENT FILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 5450

SOFTWARE: Patentin version 3.0

SEQ ID NO 5415

LENGTH: 15

TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-927-046-5415

Query Match 88.2%; Score 15; DB 10; Length 15;  
Best Local Similarity 60.0%; Pred. No. 4.4e+02;  
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 3 UGAUUCAGGCA 17  
:|::|::|::|  
DB 1 TGATTTCATTGCG 15

RESULT 7  
US-09-927-046-141

Sequence 141, Application US/09927046  
Publication No. US20030064946A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc

APPLICANT: MCSwigen, Jim

APPLICANT: Thompson, Jim

APPLICANT: McKenzie, Tim

APPLICANT: Ayers, Dave

APPLICANT: Grupe, Andrew

APPLICANT: Szymowski, Edmund

TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloro

FILE REFERENCE: 249/021

CURRENT APPLICATION NUMBER: US/09/927,046

CURRENT FILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 5450

SOFTWARE: Patentin version 3.0

SEQ ID NO 141

LENGTH: 17

TYPE: RNA

ORGANISM: Homo sapiens  
US-09-927-046-141

Query Match 88.2%; Score 15; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUAGUUUCAGGCA 15  
|||::|::|::|  
DB 3 CCGAUUUCAGGCA 17

RESULT 8  
US-09-864-761-32170

Sequence 32170, Application US/09864761  
Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: Aecm1ca-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 32170  
LENGTH: 88  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC010087.2  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.89  
OTHER INFORMATION: SWISSPROT HIT: P38650, EVALU6.00e-03  
OTHER INFORMATION: NT HIT: X95966.1, EVALU6.7.20e-01  
OTHER INFORMATION: EST\_HUMAN HIT: A1707484.1, EVALU6.1.70e-02  
US-09-864-761-32170

Query Match 88.2%; Score 15; DB 9; Length 88;  
Best Local Similarity 60.0%; Pred. No. 5.8e+02;  
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAUTCACUUGCA 15  
DB 63 CCTGATTCATTGCA 77

RESULT 9  
US-10-719-900-534802/c  
Sequence 534802, Application US/10719900  
Publication No. US20050026164A1  
GENERAL INFORMATION:  
APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
FILE REFERENCE: 3528.1  
CURRENT APPLICATION NUMBER: US/10/719,900  
CURRENT FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: 60/427,808  
PRIOR FILING DATE: 2002 11 20  
NUMBER OF SEQ ID NOS: 982914  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 534802  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-719-900-534802

Query Match 84.7%; Score 14.4; DB 10; Length 25;  
Best Local Similarity 62.5%; Pred. No. 1e+03;  
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 CUGAUTCACUUGCAGG 17  
DB 22 CTGATTCATTGCAAG 7

RESULT 10  
US-09-927-046-5412  
Sequence 5412, Application US/09927046  
Publication No. US20030064946A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc  
APPLICANT: McSwiggen, Jim  
APPLICANT: Thompson, Jim  
APPLICANT: McKenzie, Tim  
APPLICANT: Ayers, Dave  
APPLICANT: Grupe, Andrew  
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric  
TITLE OF INVENTION: Channel-1  
FILE REFERENCE: 249/021  
CURRENT APPLICATION NUMBER: US/09/927,046  
CURRENT FILING DATE: 2001-08-09  
NUMBER OF SEQ ID NOS: 5450  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5412  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-927-046-5412

Query Match 82.4%; Score 14; DB 10; Length 15;  
Best Local Similarity 57.1%; Pred. No. 1.5e+03;  
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAUTCACUUGC 14  
DB 2 CCTGATTCATTGTC 15

RESULT 11  
US-09-927-046-144  
Sequence 144, Application US/09927046  
Publication No. US20030064946A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc  
APPLICANT: McSwiggen, Jim  
APPLICANT: Thompson, Jim  
APPLICANT: McKenzie, Tim  
APPLICANT: Ayers, Dave  
APPLICANT: Grupe, Andrew  
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric  
TITLE OF INVENTION: Channel-1  
FILE REFERENCE: 249/021  
CURRENT APPLICATION NUMBER: US/09/927,046  
CURRENT FILING DATE: 2001-08-09  
NUMBER OF SEQ ID NOS: 5450  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 144  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-927-046-144

Query Match 82.4%; Score 14; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAUUTCACUUGCAGG 17  
DB 1 GAUUTCACUUGCAGG 14

RESULT 12

US-10-481-613-159/c  
 ; Sequence 159, Application US/10481613  
 ; Publication No. US20050085627A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhang, Youming  
 ; APPLICANT: Moffatt, Miriam  
 ; APPLICANT: Cookson, William  
 ; APPLICANT: Tinsley, Jon  
 ; TITLE OF INVENTION: Atopy  
 ; FILE REFERENCE: 16721-0003US1 / P32688W0/KVC  
 ; CURRENT APPLICATION NUMBER: US/10/481,613  
 ; CURRENT FILING DATE: 2003-12-19  
 ; PRIOR APPLICATION NUMBER: PCT/GB02/02859  
 ; PRIOR FILING DATE: 2002-06-21  
 ; PRIOR APPLICATION NUMBER: GB 015211.5  
 ; PRIOR FILING DATE: 2001-06-21  
 ; PRIOR APPLICATION NUMBER: GB 015212.3  
 ; PRIOR FILING DATE: 2001-06-21  
 ; PRIOR APPLICATION NUMBER: GB 015213.1  
 ; PRIOR FILING DATE: 2001-06-21  
 ; NUMBER OF SEQ ID NOS: 326  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 159  
 ; LENGTH: 19  
 ; TYPE: DNA  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Primer  
 ; US-10-481-613-159

Query Match 82.4%; Score 14; DB 19; Length 19;  
 Best Local Similarity 64.3%; Pred. No. 1.6e+03;  
 Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAUUCAUUGCAG 17  
 ||::||::||::||  
 Db 19 GATTTCATTGCGAG 6

RESULT 13  
 US-10-719-900-922893/c  
 ; Sequence 922893, Application US/10719900  
 ; Publication No. US20050026164A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
 ; FILE REFERENCE: 3528.1  
 ; CURRENT APPLICATION NUMBER: US/10/719,900  
 ; CURRENT FILING DATE: 2003-11-20  
 ; PRIOR APPLICATION NUMBER: 60/427,808  
 ; PRIOR FILING DATE: 2002-11-20  
 ; NUMBER OF SEQ ID NOS: 982914  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 922893  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 ; US-10-719-900-922893

Query Match 82.4%; Score 14; DB 19; Length 25;  
 Best Local Similarity 57.1%; Pred. No. 1.7e+03;  
 Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 3 UGAUUUCAUUGCAG 16  
 :||::||::||::||  
 Db 21 TGAATTTCATTGCGAG 8

RESULT 14  
 US-10-719-900-716006/c  
 ; Sequence 716006, Application US/10719900  
 ; Publication No. US20050026164A1  
 ; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
 ; FILE REFERENCE: 3528.1  
 ; CURRENT APPLICATION NUMBER: US/10/719,900  
 ; CURRENT FILING DATE: 2003-11-20  
 ; PRIOR APPLICATION NUMBER: 60/427,808  
 ; PRIOR FILING DATE: 2002-11-20  
 ; NUMBER OF SEQ ID NOS: 982914  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 716006  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 ; US-10-719-900-716006

Query Match 81.2%; Score 13.8; DB 19; Length 25;  
 Best Local Similarity 58.8%; Pred. No. 2.1e+03;  
 Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAUUGCAG 17  
 ||::||::||::||  
 Db 23 CCTGAATTTCATTGCGCG 7

RESULT 15  
 US-10-004-219B-12  
 ; Sequence 12, Application US/10004219B  
 ; Publication No. US20030087414A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Maciozys  
 ; APPLICANT: Aerts, Johannes M.F.G.  
 ; APPLICANT: Booc, Rolf G.  
 ; TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and  
 ; TITLE OF INVENTION: Its use in therapy or prophylaxis against diseases in  
 ; FILE REFERENCE: 2183-5136US  
 ; CURRENT APPLICATION NUMBER: US/10/004,219B  
 ; CURRENT FILING DATE: 2001-11-02  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 12  
 ; LENGTH: 22  
 ; TYPE: DNA  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: primer  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)..(22)  
 ; US-10-004-219B-12

Query Match 78.8%; Score 13.4; DB 14; Length 22;  
 Best Local Similarity 53.3%; Pred. No. 3.4e+03;  
 Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 CUGAUUUCAUUGCAG 16  
 ||::||::||::||  
 Db 8 CTGAATTTCATTGCGAG 22.

RESULT 16  
 US-10-787-845-12  
 ; Sequence 12, Application US/10787845  
 ; Publication No. US20040253224A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Maciozys  
 ; APPLICANT: Aerts, Johannes M.F.G.  
 ; APPLICANT: Booc, Rolf G.  
 ; TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and  
 ; TITLE OF INVENTION: Its use in therapy or prophylaxis against diseases in  
 ; FILE REFERENCE: 2183-5136US

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/ CURRENT APPLICATION NUMBER: US/10/787,845
/ CURRENT FILING DATE: 2004-02-26
/ PRIOR APPLICATION NUMBER: US/10/004,219
/ PRIOR FILING DATE: 2001-11-02
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 22
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: primer
/ NAME/KEY: misc.feature
/ LOCATION: (1)..(22)
US-10-787-845-12

Query Match      78.8%; Score 13.4; DB 18; Length 22;
Best Local Similarity 53.3%; Pred. No. 3.4e+03;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CUGAUUUCAUUGCAG 16
      |||:::|::|
Db      8 CTGATTTCATTGCAG 22

RESULT 17
US-10-719-900-94994
/ Sequence 94994, Application US/10719900
/ Publication No. US20050026164A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
/ FILE REFERENCE: 3528.1
/ CURRENT APPLICATION NUMBER: US/10/719,900
/ PRIOR FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,808
/ NUMBER OF SEQ ID NOS: 982914
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 94994
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-10-719-900-94994

Query Match      78.8%; Score 13.4; DB 19; Length 25;
Best Local Similarity 60.0%; Pred. No. 3.5e+03;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CUGAUUUCAUUGCAG 16
      |||:::|::|
Db      4 CAGATTTCATTGCAG 18

RESULT 18
US-10-719-900-166732
/ Sequence 166732, Application US/10719900
/ Publication No. US20050026164A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
/ FILE REFERENCE: 3528.1
/ CURRENT APPLICATION NUMBER: US/10/719,900
/ PRIOR FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,808
/ NUMBER OF SEQ ID NOS: 982914
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 166732
/ LENGTH: 25
/ TYPE: DNA
```

```
/ ORGANISM: Mus musculus
US-10-719-900-166732

Query Match      78.8%; Score 13.4; DB 19; Length 25;
Best Local Similarity 60.0%; Pred. No. 3.5e+03;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CUGAUUUCAUUGCAG 16
      |||:::|::|
Db      5 CTGATTTCATTGCAG 19

RESULT 19
US-10-719-900-220262
/ Sequence 220262, Application US/10719900
/ Publication No. US20050026164A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
/ FILE REFERENCE: 3528.1
/ CURRENT APPLICATION NUMBER: US/10/719,900
/ PRIOR FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,808
/ NUMBER OF SEQ ID NOS: 982914
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 220262
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-10-719-900-220262

Query Match      78.8%; Score 13.4; DB 19; Length 25;
Best Local Similarity 60.0%; Pred. No. 3.5e+03;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCUGAUUUCAUUGCA 15
      |||:::|::|
Db      7 CCAGATTTCATTGCA 21

RESULT 20
US-10-719-900-912524
/ Sequence 912524, Application US/10719900
/ Publication No. US20050026164A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
/ FILE REFERENCE: 3528.1
/ CURRENT APPLICATION NUMBER: US/10/719,900
/ PRIOR FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,808
/ NUMBER OF SEQ ID NOS: 982914
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 912524
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-10-719-900-912524

Query Match      78.8%; Score 13.4; DB 19; Length 25;
Best Local Similarity 60.0%; Pred. No. 3.5e+03;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCUGAUUUCAUUGCA 15
      |||:::|::|
Db      11 CCTGAATTCATTGCA 25

RESULT 21
US-10-809-189-54192/c
/ Sequence 54192, Application US/10809189
```

Publication No. US20050048531A1  
GENERAL INFORMATION:  
APPLICANT: Michael Wittmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/10/809,189  
CURRENT FILING DATE: 2004-03-25  
PRIOR APPLICATION NUMBER: US/09/396,196  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 54192  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-10-809-189-54192

Query Match 78.8%; Score 13.4; DB 19; Length 25;  
Best Local Similarity 53.3%; Pred. No. 3.5e+03;  
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGAVUUCAUUGCAGG 17  
DB 25 TGCTTCATTGCAGG 11

RESULT 22  
US-10-809-189-60898  
Sequence 60898, Application US/10809189  
Publication No. US20050048531A1

GENERAL INFORMATION:  
APPLICANT: Michael Wittmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/10/809,189  
CURRENT FILING DATE: 2004-03-25  
PRIOR APPLICATION NUMBER: US/09/396,196  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 60898  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-10-809-189-60898

Query Match 78.8%; Score 13.4; DB 19; Length 25;  
Best Local Similarity 53.3%; Pred. No. 3.5e+03;  
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCUGAUCUUCAUUGCA 15  
DB 10 CCGATTCATTGAA 24

RESULT 23  
US-10-445-789-17/c  
Sequence 17, Application US/10445789  
Publication No. US20030232418A1  
GENERAL INFORMATION:  
APPLICANT: TAKESHIWA, Seiji  
APPLICANT: SOGABE, Atsushi  
APPLICANT: OKA, Masanori

TITLE OF INVENTION: MODIFIED PYROLOQUINOLINE QUINONE (PQQ) DEPENDENT GLUCOSE  
TITLE OF INVENTION: DEHYDROGENASE WITH SUPERIOR SUBSTRATE SPECIFICITY AND STABILITY  
FILE REFERENCE: 222927  
CURRENT APPLICATION NUMBER: US/10/445,789  
CURRENT FILING DATE: 2003-05-27  
PRIOR APPLICATION NUMBER: JP 2002-152911  
PRIOR FILING DATE: 2002-05-27  
PRIOR APPLICATION NUMBER: JP 2002-152913  
PRIOR FILING DATE: 2002-05-27  
PRIOR APPLICATION NUMBER: JP 2003-080244  
PRIOR FILING DATE: 2003-03-24  
PRIOR APPLICATION NUMBER: JP 2003-080310  
PRIOR FILING DATE: 2003-03-24  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 17  
LENGTH: 52  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
NAME/KEY: misc\_feature  
LOCATION: (18)..(26)  
OTHER INFORMATION: page 43, line 2 from the bottom  
US-10-445-789-17

Query Match 78.8%; Score 13.4; DB 17; Length 52;  
Best Local Similarity 53.3%; Pred. No. 3.9e+03;  
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGAVUUCAUUGCAGG 17  
DB 15 TGATTGATTGCAGG 1

RESULT 24  
US-09-927-046-5416  
Sequence 5416, Application US/09927046  
Publication No. US20030064946A1

GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc  
APPLICANT: McSwiggen, Jim  
APPLICANT: Thompson, Jim  
APPLICANT: McKenzie, Tim  
APPLICANT: Ayers, Dave  
APPLICANT: Grupe, Andrew  
APPLICANT: Szymkowski, Edmund  
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric  
TITLE OF INVENTION: Channel-1  
FILE REFERENCE: 249/021  
CURRENT APPLICATION NUMBER: US/09/927,046  
CURRENT FILING DATE: 2001-08-09  
NUMBER OF SEQ ID NOS: 5450  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5416  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-927-046-5416

Query Match 76.5%; Score 13; DB 10; Length 15;  
Best Local Similarity 61.5%; Pred. No. 5.3e+03;  
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 5 AUUCAUUGCAGG 17  
DB 1 ATTTCATTGCAGG 13

RESULT 25

US-10-839-688-70/c  
; Sequence 70, Application US/10839688  
; Publication No. US20050014173A1  
; GENERAL INFORMATION:  
; APPLICANT: Farter, Matthew J.  
; TITLE OF INVENTION: PARKINSON'S DISEASE MARKERS  
; FILE REFERENCE: 07039-448001  
; CURRENT APPLICATION NUMBER: US/10/839,688  
; CURRENT FILING DATE: 2004-05-05  
; PRIOR APPLICATION NUMBER: US 60/468,832  
; PRIOR FILING DATE: 2003-05-08  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 70  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-839-688-70

Query Match 76.5%; Score 13; DB 19; Length 15;  
Best Local Similarity 46.7%; Pred. No. 5.3e+03;  
Matches 7; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 3 UGAUUCAUUGCAGG 17  
; :||:::|||  
Db 15 TTATTCTTGCAGG 1

RESULT 26  
US-09-927-046-1247  
; Sequence 1247, Application US/09927046  
; Publication No. US20030064946A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc  
; APPLICANT: McSwigen, Jim  
; APPLICANT: Thompson, Jim  
; APPLICANT: Mckenzie, Tim  
; APPLICANT: Ayers, Dave  
; APPLICANT: Grupe, Andrew  
; APPLICANT: Szymkowski, Edmund  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori  
; FILE REFERENCE: 249/021  
; CURRENT APPLICATION NUMBER: US/09/927,046  
; CURRENT FILING DATE: 2001-08-09  
; NUMBER OF SEQ ID NOS: 5450  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1247  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-927-046-1247

Query Match 76.5%; Score 13; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AUUUCAUUGCAGG 17  
; |||||  
Db 1 AUUUCAUUGCAGG 13

RESULT 27  
US-09-927-046-1671  
; Sequence 1671, Application US/09927046  
; Publication No. US20030064946A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc  
; APPLICANT: McSwigen, Jim  
; APPLICANT: Thompson, Jim  
; APPLICANT: Mckenzie, Tim  
; APPLICANT: Ayers, Dave  
; APPLICANT: Grupe, Andrew

; APPLICANT: Szymkowski, Edmund  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric  
; FILE REFERENCE: 249/021  
; CURRENT APPLICATION NUMBER: US/09/927,046  
; CURRENT FILING DATE: 2001-08-09  
; NUMBER OF SEQ ID NOS: 5450  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1671  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-927-046-1671

Query Match 76.5%; Score 13; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCUGAUUUCAUUG 13  
; |||||  
Db 5 CCUGAUUUCAUUG 17

RESULT 28  
US-10-719-900-360099  
; Sequence 360099, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 360099  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-360099

Query Match 76.5%; Score 13; DB 19; Length 25;  
Best Local Similarity 53.8%; Pred. No. 5.7e+03;  
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CUGAUUUCAUUGC 14  
; |||||  
Db 11 CTGATTCATTGC 23

RESULT 29  
US-10-719-900-491812  
; Sequence 491812, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 491812  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-491812

Query Match 76.5%; Score 13; DB 19; Length 25;

Best Local Similarity 53.8%; Pred. No. 5.7e+03;  
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCUGAUNUCG 14  
Db 10 CCGATTTCATTG 22

## RESULT 30

US-10-719-900-813289  
; Sequence 813289, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Method of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; PRIOR FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; NUMBER OF SEQ ID NOS: 11 20  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 813289  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-813289

Query Match 76.5%; Score 13; DB 19; Length 25;  
Best Local Similarity 53.8%; Pred. No. 5.7e+03;  
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAUNUCG 13  
Db 12 CCGATTTCATTG 24

## RESULT 31

US-10-809-189-119128/c  
; Sequence 119128, Application US/10809189  
; Publication No. US2005004851A1  
; GENERAL INFORMATION:  
; APPLICANT: Michael Miltmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/10/809,189  
; PRIOR FILING DATE: 2004-03-25  
; CURRENT APPLICATION NUMBER: US/09/396,196  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 119128  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-10-809-189-119128

Query Match 76.5%; Score 13; DB 19; Length 25;  
Best Local Similarity 53.8%; Pred. No. 5.7e+03;  
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 3 UGAUUCAUUGCA 15  
Db 25 TGAATTCATTGCA 13

## RESULT 32

US-10-741-849-1206/c

; Sequence 1206, Application US/10741849  
; Publication No. US20050019931A1  
; GENERAL INFORMATION:  
; APPLICANT: Roemer, Terry  
; APPLICANT: Jiang, Bo  
; APPLICANT: Boone, Charles  
; APPLICANT: Bussey, Howard  
; TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of

; FILE REFERENCE: 10182-023-999  
; CURRENT APPLICATION NUMBER: US/10/741,849  
; PRIOR FILING DATE: 2003-12-19  
; PRIOR APPLICATION NUMBER: US 60/434,832  
; PRIOR FILING DATE: 2002-12-19  
; NUMBER OF SEQ ID NOS: 8000  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1206  
; LENGTH: 43  
; TYPE: DNA  
; ORGANISM: Candida albicans  
US-10-741-849-1206

Query Match 76.5%; Score 13; DB 19; Length 43;  
Best Local Similarity 53.8%; Pred. No. 6.2e+03;  
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAUNUCG 13  
Db 22 CCGATTTCATTG 10

## RESULT 33

US-09-908-975-18678  
; Sequence 18678, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FRISHER, Simchon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; PRIOR FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 18678  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-908-975-18678

Query Match 76.5%; Score 13; DB 10; Length 60;  
Best Local Similarity 61.5%; Pred. No. 6.5e+03;  
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAUUCAUUGCAG 16  
Db 30 GAATTCATTGCG 42

## RESULT 34

US-10-751-736-12517/c  
; Sequence 12517, Application US/10751736  
; Publication No. US20040265230A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth

```

; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12517
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-12517

Query Match
Best Local Similarity 75.3%; Score 12.8; DB 18; Length 21;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CUGAUVUUCAUUGCAGG 17
Db 18 CTGATTCCTTGTAGG 3

RESULT 35
US-10-751-736-12518/c
; Sequence 12518, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12518
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-12518

Query Match
Best Local Similarity 75.3%; Score 12.8; DB 18; Length 21;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CUGAUVUUCAUUGCAGG 17
Db 16 CTGATTCCTTGTAGG 1

RESULT 36
US-10-098-263B-108838
; Sequence 108838, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
```

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; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 108838
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-108838

Query Match
Best Local Similarity 75.3%; Score 12.8; DB 15; Length 25;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCUGAUVUUCAUUGCAGG 16
Db 9 CCAGATTCATTGAAG 24

RESULT 37
US-10-719-900-134100/c
; Sequence 134100, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 134100
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-134100

Query Match
Best Local Similarity 75.3%; Score 12.8; DB 19; Length 25;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCUGAUVUUCAUUGCAGG 16
Db 17 CCGATTCCTTGTAGG 2

RESULT 38
US-10-719-900-200558
; Sequence 200558, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 200558
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-200558

Query Match
Best Local Similarity 75.3%; Score 12.8; DB 19; Length 25;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CUGAUVUUCAUUGCAGG 17
Db 7 CTGATTCCTTGTAGG 22
```

```

RESULT 39
US-10-719-900-220971
; Sequence 220971, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 220971
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-220971

```

```

Query Match      75.3%; Score 12.8; DB 19; Length 25;
Best Local Similarity 50.0%; Pred.No.7.3e+03;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      1 CCUGAUUUCAGUCAG 16
      ||:|::|::|::|
Db      5 CCTATTATTATCGCAG 20

```

```

RESULT 40
US-10-719-900-220972
; Sequence 220972, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 220972
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-220972

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Query Match      75.3%; Score 12.8; DB 19; Length 25;
Best Local Similarity 50.0%; Pred.No.7.3e+03;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 CCUGAUUUCAGUCAG 16
      ||:|::|::|::|
Db      5 CCTATTATTATCGCAG 20

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Search completed: May 13, 2005, 18:25:00  
 Job time : 147.964 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2005, 16:42:23 ; Search time 827.127 Seconds  
(without alignments)  
782.337 Million cell updates/sec

Title: US-09-927-046-143

Perfect score: 17

Sequence: 1 ccgaauuacaucaagcagg 17

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 675282

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hic: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gss1: \*  
9: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
C 1	14.4	84.7	73 5	BQ595072 E012708-0
C 2	13.4	78.8	66 7	D20621 HUMG01596
C 3	13.4	78.8	87 7	CO900072 Mdbb5020E
C 4	13.4	78.8	93 9	DR1SE1T
C 5	13.4	78.8	94 1	AI604455 mu20h07.y
C 6	13.4	78.8	97 7	CK098392 A013P34.5
C 7	13.4	78.8	82 2	BF506915 116P-26
C 8	12.8	75.3	52 2	BE317163 NF069A05L
C 9	12.8	75.3	60 2	BE249419 NF019A03L
C 10	12.8	75.3	61 7	CN866036 000907AAL
C 11	12.8	75.3	69 1	AA816117 VP56h06.r
C 12	12.8	75.3	71 9	CR170276 ReverseB.r
C 13	12.8	75.3	75 8	CC459199 SALK_1261
C 14	12.8	75.3	77 2	BE316157 NF029F07L
C 15	12.8	75.3	85 1	AL847774 AL847774
C 16	12.8	75.3	88 7	CK108729 1064P85.P
C 17	12.8	75.3	89 1	AA616611 VO13B01.r
C 18	12.8	75.3	89 9	CG721352 1119066E1
C 19	12.4	72.9	40 1	AA948148 on51F04.s
C 20	12.4	72.9	50 8	BZ594604 SALK_0845
C 21	12.4	72.9	54 1	AA760149 vV70D11.r
C 22	12.4	72.9	61 8	AZ762535 1M0557G06
C 23	12.4	72.9	61 8	CL528748 ASV7F11.f
C 24	12.4	72.9	63 8	BH866175 SALK_1008

C 25	12.4	72.9	65 9	CR769964 Arabidops
C 26	12.4	72.9	65 9	CG606249 OST283929
C 27	12.4	72.9	67 1	AL853876 AL853876
C 28	12.4	72.9	74 4	BM514574 KY05D03.y
C 29	12.4	72.9	74 8	AZ468373 1M0281A22
C 30	12.4	72.9	77 8	BZ593321 SALK_0700
C 31	12.4	72.9	79 2	AM672652 1X Exp1an
C 32	12.4	72.9	80 5	B0925856 Bae83A10.
C 33	12.4	72.9	81 8	AZ339200 1M0070M06
C 34	12.4	72.9	82 8	BZ587139 3590.1.10
C 35	12.4	72.9	83 7	CN855612 000721AAA
C 36	12.4	72.9	83 8	BH791384 SALK_0598
C 37	12.4	72.9	91 8	AZ820505 2M0522P06
C 38	12.4	72.9	96 6	CV296295 EST884672
C 39	12.4	72.9	96 6	BI090229 602857182
C 40	12.4	72.9	98 4	CF035704 OCG21C02.
C 41	12.4	72.9	100 6	CF035704 OCG21C02.
C 42	12.2	71.8	52 9	CR178995 ReverseB.r
C 43	12.2	71.8	57 9	CG720057 1119060D1
C 44	12.2	71.8	57 1	AA237647 mx28g09.r
C 45	12.2	71.8	67 7	CF974344 Psu_np11\
C 46	12.2	71.8	68 9	AJ588170 Arabidops
C 47	12.2	71.8	71 7	CK106624 UB27CPB08
C 48	12.2	71.8	76 7	CK101897 F130P37.5
C 49	12.2	71.8	77 1	AI960062 BC37F04.x
C 50	12.2	71.8	77 9	CG816675 100002F18
C 51	12.2	71.8	78 1	AA197575 mu18C10.r
C 52	12.2	71.8	78 9	CG571027 CH240.446
C 53	12.2	71.8	83 9	CG522312 OST91.791
C 54	12.2	71.8	83 9	CG668947 OST465406
C 55	12.2	71.8	85 1	AA733618 VA74802.r
C 56	12.2	71.8	86 1	AI493964 q252D10.x
C 57	12.2	71.8	87 6	CA819137 Bae69E10.
C 58	12.2	71.8	89 7	D19064 MUSGS01271
C 59	12.2	71.8	90 2	AM059654 AhuTh.bae
C 60	12.2	71.8	91 2	AW733398 BK73A03.y
C 61	12.2	71.8	91 5	BK728604 BK728604
C 62	12.2	71.8	91 9	AL938041 Arabidops
C 63	12.2	71.8	96 9	CG615636 OST306533
C 64	12.2	71.8	97 1	AI318243 LB12C04.x
C 65	12.2	71.8	98 9	CC817050 100002F18
C 66	12.2	70.6	51 6	CB225639 1RT19G03
C 67	12.2	70.6	67 9	AL241968 Tetradon
C 68	12.2	70.6	74 9	CC555952 CH240.463
C 69	12.2	70.6	76 2	BF642720 NF070E011
C 70	12.2	70.6	77 1	AI035461 ub47C09.r
C 71	12.2	70.6	77 1	AI035461 ub47C09.r
C 72	12.2	70.6	85 8	BZ593006 SALK_0550
C 73	12.2	70.6	85 9	CG628190 OST359110
C 74	12.2	70.6	94 4	BM178932 B6161C04.
C 75	12.2	70.6	98 1	AA625055 A66EF05.r
C 76	12.2	70.6	98 4	BJ064688 BJ064688
C 77	12.2	70.6	34 1	AA953692 on88d01.8
C 78	11.8	69.4	53 7	R88455 ym92d07.r1
C 79	11.8	69.4	54 4	BJ053682 BJ053682
C 80	11.8	69.4	56 9	AL769433 Arabidops
C 81	11.8	69.4	57 9	CR144689 Forward.s
C 82	11.8	69.4	58 7	D18271 MUSGS00467
C 83	11.8	69.4	58 9	CR088089 Forward.s
C 84	11.8	69.4	61 8	AZ482837 1M0308B09
C 85	11.8	69.4	61 8	AI440949 B655509.y
C 86	11.8	69.4	64 1	AU052007 A0052007
C 87	11.8	69.4	64 9	CG634159 OST354779
C 88	11.8	69.4	65 9	CG620109 OST316815
C 89	11.8	69.4	66 8	BH613007 SALK_0336
C 90	11.8	69.4	73 9	CR074033 Forward.B
C 91	11.8	69.4	75 1	AA702075 ZT90E02.r
C 92	11.8	69.4	75 5	BU870046 Q007E08.P
C 93	11.8	69.4	76 6	CB923183 VVD093B02
C 94	11.8	69.4	76 9	CG569409 OST197477
C 95	11.8	69.4	77 9	AG193769 Pan.trog1
C 96	11.8	69.4	78 9	CG569373 OST197379
C 97	11.8	69.4	80 1	AI357487 qu01g09.x

98 11.8 69.4 80 8 CC178575 CC178575 NPX400 Ba  
 c 99 11.8 69.4 81 1 AA980013 AA980013 DDS8 Pea  
 c 100 11.8 69.4 84 1 AT719989 AT719989 aa848c11.x

## ALIGNMENTS

RESULT 1  
 BOS95072/c 73 bp mRNA linear EST 06-DEC-2002  
 LOCUS E012708-024-023-E15-SP6 MP12-ADIS-024-developing root Beta vulgaris  
 DEFINITION CDNA clone 024-023-E15 5-PRIME, mRNA sequence.  
 ACCESSION BQ595072  
 VERSION BQ595072.1 GI:26124655  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 73)  
 Herrig,R.; Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,U., Lehrach,H.  
 and Radloff,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)  
 22362189  
 12472698

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT

ADIS DNA core facility at MP12  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mp12-koeln.mpg.de  
 Insert Length: 73 Std Error: 0.00  
 Plate: 23 row: B column: 15  
 Seq primer: SP6; CATACGATTGATGACACTATAG.  
 Location/Qualifiers  
 1..73  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KMS2320 (double haploid, monogerm breeding  
 line)"  
 /db\_xref="GABI:191784"  
 /db\_xref="taxon:161934"  
 /clone="024-023-E15"  
 /tissue\_type="developing root"  
 /lab\_host="EMDH10B"  
 /clone\_lib="MP12-ADIS-024-developing root"  
 /note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KMS  
 Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
 orientation:  
 SP6-sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

## ORIGIN

Query Match 84.7%; Score 14.4; DB 5; Length 73;  
 Best Local Similarity 56.2%; Pred. No. 8e+03; 1; Indels 0; Gaps 0;  
 Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CCUGAUCUUCAGCAG 16  
 ||:||||:||||  
 Db 35 CCTATTTCATGCGAG 20

RESULT 2

D20621/c 66 bp mRNA linear EST 30-JUL-1996  
 LOCUS HUMG501596 Human promyelocyte Homo sapiens cDNA pm0560 3',  
 DEFINITION mRNA sequence.  
 ACCESSION D20621  
 VERSION D20621.1 GI:501717  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 66)  
 Okubo,K., Fukushima,A., Yoshii,J., Niijima,T., Kojima,Y.,  
 Yoshinari,H., Arimoto,J. and Matsubara,K.  
 Gene expression of human promyelocytic cell line HL60 before and  
 after induction of differentiation. A new application of 3'directed  
 cDNA sequencing  
 Unpublished (1993)

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Unpublished (1993)  
 Contact: Okubo,K., Fukushima,A., Yoshii,J., Niijima,T., Kojima,Y.,  
 Yoshinari,H., Arimoto,J. and Matsubara,K.  
 Institute for Molecular and Cellular Biology  
 Osaka University  
 3-1 Yamada-oka, Suita, Osaka 565, Japan.  
 Location/Qualifiers  
 1..66  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="pm0560"  
 /clone\_lib="Human promyelocyte"  
 /note="Female, adult, cell\_line = HL60, cell\_type =  
 promyelocyte."

## ORIGIN

Query Match 78.8%; Score 13.4; DB 7; Length 66;  
 Best Local Similarity 53.3%; Pred. No. 2.7e+04;  
 Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Oy 3 UGAUUCUUCAGCAG 17  
 :||:||||:  
 Db 54 TGATTTATTCGAG 40

RESULT 3  
 CO900072/c 87 bp mRNA linear EST 13-AUG-2004  
 LOCUS Mddb5020f11.y1 Mddb Malus x domestica cDNA clone Mddb5020f11 5',  
 DEFINITION mRNA sequence.  
 ACCESSION CO900072  
 VERSION CO900072.1 GI:51239862  
 KEYWORDS EST.  
 SOURCE Malus x domestica (cultivated apple)  
 ORGANISM Malus x domestica

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.  
 1 (bases 1 to 87)  
 Korban,S., Vodka,L., Liu,L., Gasic,K., Gonzales,O., Hernandez,A.,  
 Aldwinckle,H., Malnoy,M., Carroll,N., Goldbrough,P., Orya,K.,  
 Clifton,S., Page,D., Marra,M., Hillier,L., Martin,J., Wylie,T.,  
 Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Ronko,I.,  
 Tsagarisvili,R., Kennedy,S., Waterson,R. and Wilson,R.  
 Apple Functional Genomics grant - NSF 0321702  
 Unpublished (2004)

Contact: Schnyler S. Korban  
 Apple Functional Genomics grant - NSF 0321702  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Library materials provided by: Schnyler S. Korban Library  
 constructed by: K. Gasic Library sequenced by: Washington

University Genome Sequencing Center  
Washu EST name: aa23c06.y1  
Seq primer: -40UP from Gibco.  
Location/Qualifiers

## FEATURES

source

1. 87  
/organism="Mus mus domestica"  
/mol\_type="mRNA"  
/cultivar="Goldrush"  
/db\_xref="taxon:3750"  
/clone="Mdb5020f11"  
/lab\_host="DHI08 amplicillin resistant"  
/clone\_lib="Mdbb"

/note="Vector: Bluescript II SK (+); Site 1: NotI, Site 2: EcoRII; Total RNA was extracted separately from each stage (dormant terminal bud, dormant lateral bud, active lateral bud), using the 'pine tree' method. Poly(A)+mRNA was isolated twice from total RNA from each stage using the Oligotex Direct mRNA kit (Qiagen). mRNA was reverse transcribed into double stranded cDNA using a modified oligo18(dt) primer with an identifying tag sequence (see table below). cDNAs from different stages were pooled in equal amounts before adaptor ligation. Tag identification when sequencing from 5' end: Stage 1 (dormant terminal bud) insert 18(A)TCGTG; Stage 2 (dormant lateral bud) insert 18(A)TCGTG; Stage 3 (active lateral bud) insert 18(A)TCGTG; Tag identification when sequencing from 3' end: Stage 1 (dormant terminal bud) CACGA18(T) insert; Stage 2 (dormant lateral bud) CACGA18(T) insert; Stage 3 (active lateral bud) ACCGA18(T) insert; Double stranded cDNAs were size selected (more than 450 bp), adapted with EcoRI adaptors at both ends and then digested with NotI. The cDNAs were then directionally cloned into EcoRI-NotI digested pBS II SK(+) phagemid vector (Stratagene). Identification of adaptors and tags in 5'-end sequenced clones: <Vector>..TAACTT<End Vector><Start EcoRI adaptor>GATTCGATTCGATTCGCGG<End EcoRI adaptor><Start insert>..AAAAAAAAAAAAAAAAA<End insert><Start Tag>TCGA<End Tag><Start NotI site>Vector>GCGCGCGCACCGCGG.. The total number of white colony forming units (cfu) in the primary library before amplification was 4x10<sup>5</sup> cfu (colony forming units). The background of empty clones was less than 10%. Inserts ranged from 0.5 kb to 4 kb, as determined by PCR. Purified plasmid DNA from the primary library was converted to single-stranded circles and used as a template for PCR amplification using the T7 and T3 priming sites flanking the cloned cDNA inserts. The purified PCR products, representing the entire cloned cDNA population, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 h at 30C. Unhybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DHI08 cells to generate the normalized library. The total number of clones with insert was 1x10<sup>6</sup> cfu. Background of empty clones was less than 2%.

## ORIGIN

Query Match 78.8%; Score 13.4; DB 7; Length 87;  
Best Local Similarity 53.3%; Pred. No. 2.8e+04;  
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 CUGAUCUUCAG 16  
DB 46 CTGATTCATTGCGG 32

RESULT 4  
LOCUS DRI15E15T 93 bp DNA linear GSS 27-NOV-2002  
DEFINITION Dario rerio genomic clone DKEX-15E15, genomic survey sequence.  
ACCESSION AL747314  
VERSION AL747314.1 GI:21343670

KEYWORDS  
SOURCE  
ORGANISM

GSS.  
Dario rerio (zebrafish)  
Dario rerio

## REFERENCE

AUTHORS Humphrey, S.J., Huckle, E. and Hunt, S.E.  
TITLE Direct Submission  
JOURNAL Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humphrey@sanger.ac.uk Unpublished

## COMMENT

This sequence was generated from the T7 end of BAC 15E15. 15E15 is part of the Dariokey BAC library created by R. Plaetk and N.V. Keygene.  
Further details: [http://www.sanger.ac.uk/Projects/D\\_rerio/](http://www.sanger.ac.uk/Projects/D_rerio/).

## FEATURES

source

1. 93  
/organism="Dario rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKEX-15E15"  
/tissue\_type="Testis"  
/note="vector pindigobAC-536"

## ORIGIN

Query Match 78.8%; Score 13.4; DB 9; Length 93;  
Best Local Similarity 53.3%; Pred. No. 2.9e+04;  
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 3 CUGAUCUUCAG 17  
DB 40 TCAATTCATTGAAG 26

## RESULT 5

LOCUS A1604455 94 bp mRNA linear EST 21-APR-1999  
DEFINITION mu20h07.y1 Soares\_thymus\_2ndMT Mus musculus cDNA clone IMAGE:639997

ACCESSION A1604455.1 GI:4613622  
VERSION A1604455.1  
KEYWORDS

SOURCE Mus musculus (house mouse)  
ORGANISM

## REFERENCE

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 94)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

## JOURNAL

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgsbbs-remail.nih.gov

## COMMENT

This clone is available royalty-free through LINT; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information. This read has been verified (found to hit its original self in the correct orientation)  
Seq primer: -40RP from Gibco  
High quality sequence stop: 57.  
Location/Qualifiers

## FEATURES

source

1. 94  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="CS7BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:639997"  
/sex="male"  
/tissue\_type="thymus"  
/dev\_stage="4 weeks"  
/lab\_host="DHI08"  
/clone\_lib="Soares\_thymus\_2ndMT"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCATCTGAGTGGAGCGCGGGTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 78.8%; Score 13.4; DB 1; Length 94;  
Best Local Similarity 53.3%; Pred. No. 2.9e+04;  
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGAAUUCAGCAGG 17  
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50 TGATTTCATTCAGG 64

## RESULT 6

CK098392 97 bp mRNA linear EST 01-DEC-2003  
LOCUS A013P34.5pr Hybrid aspen plasmid library Populus tremula x Populus  
DEFINITION tremuloideis cDNA clone A013P34 5', mRNA sequence.  
CK098392  
ACCESSION CK098392.1 GI:36582717  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Populus tremula x Populus tremuloideis  
Populus tremula x Populus tremuloideis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.  
1 (bases 1 to 97)  
Stekky,F., Bhalerao,R.R., Unneberg,P., Segerman,B., Nilsson,P.,  
Brunner,A.M., Campaa,L., Jonsson-Lindvall,J., Tandre,K.,  
Struss,S.H., Sundberg,B., Gustafsson,P., Uhlen,M., Bhalerao,R.P.,  
Nilsson,O., Sandberg,G., Karlsson,J., Lundberg,J. and Jansson,S.  
A Populus EST resource for functional genomics  
Unpublished (2003)

## REFERENCE

## AUTHORS

TITLE  
JOURNAL  
COMMENT

## ORIGIN

Query Match 78.8%; Score 13.4; DB 1; Length 94;  
Best Local Similarity 53.3%; Pred. No. 2.9e+04;  
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 CUGAUUUCAGCAG 16  
:|||||:|||||

CK098392 97 bp mRNA linear EST 01-DEC-2003  
LOCUS A013P34.5pr Hybrid aspen plasmid library Populus tremula x Populus  
DEFINITION tremuloideis cDNA clone A013P34 5', mRNA sequence.  
CK098392  
ACCESSION CK098392.1 GI:36582717  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Populus tremula x Populus tremuloideis  
Populus tremula x Populus tremuloideis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.  
1 (bases 1 to 97)  
Stekky,F., Bhalerao,R.R., Unneberg,P., Segerman,B., Nilsson,P.,  
Brunner,A.M., Campaa,L., Jonsson-Lindvall,J., Tandre,K.,  
Struss,S.H., Sundberg,B., Gustafsson,P., Uhlen,M., Bhalerao,R.P.,  
Nilsson,O., Sandberg,G., Karlsson,J., Lundberg,J. and Jansson,S.  
A Populus EST resource for functional genomics  
Unpublished (2003)

## ORIGIN

Query Match 78.8%; Score 13.4; DB 7; Length 97;  
Best Local Similarity 53.3%; Pred. No. 2.9e+04;  
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 CUGAUUUCAGCAG 16  
:|||||:|||||

Db 50 CTGCTTCATTCAG 64  
||:|||||:|||||

## RESULT 7

BF506915 82 bp mRNA linear EST 07-DEC-2000  
LOCUS 116P-26 Pooled green leaf and root tissue Sorghum bicolor cDNA  
DEFINITION clone 116P-26, mRNA sequence.  
BF506915  
ACCESSION BF506915.1 GI:11590213  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Sorghum bicolor (sorghum)  
Sorghum bicolor  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Sorghum.  
1 (bases 1 to 82)  
Childs,K.L., Klein,R.R., Klein,P.E., Morishige,D.T. and Mullet,J.E.  
Mapping Genes on an Integrated Sorghum Genetic and Physical Map  
Using cDNA Selection Technology  
Unpublished (2001)

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Contact: Kevin Childs  
Department of Biochemistry and Biophysics  
Texas A&M University  
College Station, TX 77843, USA  
Tel: 979 845 0832  
Fax: 979 862 4718  
Email: kchild@unix.tamu.edu.  
Location/Qualifiers

## FEATURES

## source

1..82  
/organism="Sorghum bicolor"  
/mol\_type="mRNA"  
/cullivar="BTx623"  
/db\_xref="taxon:4558"  
/clone="116P-26"  
/tissue\_type="green leaf and root tissue"  
/clone\_lib="Pooled green leaf and root tissue"  
/note="Vector: pBluescript II (SK); Site\_1: EcoRI; Site\_2:  
EcoRI"

## ORIGIN

Query Match 76.5%; Score 13; DB 2; Length 82;  
Best Local Similarity 61.5%; Pred. No. 4.6e+04;  
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 5 AUUUCAGCAGG 17  
||:|||||:|||||  
76 ATTTCATTCAGG 64

## RESULT 8

BE317163 52 bp mRNA linear EST 21-DEC-2000  
LOCUS NF069A05LF1F1033 Developing leaf Medicago truncatula cDNA clone  
DEFINITION NF069A05LF 5', mRNA sequence.  
BE317163  
ACCESSION BE317163.2 GI:11961946  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Medicago truncatula (barrel medic)  
Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
Medicago.  
1 (bases 1 to 52)  
Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,  
Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
Medicago truncatula leaf library  
Unpublished (2000)

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Contact: May GD  
On Jul 14, 2000 this sequence version replaced gi:9190940.







	RESULT	17
	LOCUS	AAG16611
Dd	DEFINITION	89 bp mRNA linear EST Oct-1997 vo13bd01.r1 Barstead mouse myotubes MPRBS Mus musculus CDNA clone IMAGE:1049737 5' similar to gpJ04173 PHOSPHOGLYCERATE MOTASE, BRAIN FORM (HUMAN) ; mRNA sequence.
	ACCESSION	AAG16611
	VERSION	
	KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)	
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 89) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubnue,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,U., Morris,M., Schellenberg,K., Stepcoe,W., Tan,F., Underwood,K., Moore,B., Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R. The WashU-HMI Mouse EST Project Unpublished (1996) Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: mousetest@watson.wustl.edu This clone is available royalty-free through LML ; contact the IMAGE Consortium ( <a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a> ) for further information. MG1:58133	
FEATURES	Trace considered overall poor quality Seq primer:-28ml3 rev2 EF from Amershams High quality sequence stop: 1. Location/Qualifiers	
SOURCE	1..89 /organism="Mus musculus" /mol_type="mRNA" /strain="C3H" /db_xref="taxon:10090" /cclone="IMAGE:1049737" /cell_line="C2C12" /lab_host="MDH108" /cloned_lib="Barstead mouse myotubes MPRBS" /vector="pT73D-Pac (Pharmacia) with a modified polylinker Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Nct I - Oligo(dT) primer [5' TGTTACAATCTGAAGTCGCGGCACCCTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTGGATCCGTG], digested with Nct I and cloned into the Nct I and Eco RI sites of the modified pT73 vector. Library constructed by Bob Barstead. The C2c12 cell line (available from ATCC, catalog # CRL-1772) differentiates rapidly, forming contractile myocytes and producing characteristic muscle proteins."	
ORIGIN	Query Match 75.3%; Score 12.8; DB 1; Length 89; Best Local Similarity 50.0%.; Pred.No. 5.9e+04;	
OY	Matches 8; Conservativity 6; Mismatches 2; Indels 0; Gaps 0;	
Db	1 CCUGAUUUCAUGCAG 16   :::   ::  27 CCTGTTTCATGTGAG 42	
RESULT	18	
	G8721352	

LOCUS	CG212352	89 bp	DNA	linear	SSS 20-OCT-2003
DEFINITION	1119066E12.Y1 1119 - Rescemu Grid AA Zea mays genomic, genomic survey sequence.				
ACCESSION	CG212352				
VERSION	CG212352.1	GI:37755139			
KEYWORDS	SSS.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 89)				
TITLE	Maize genomic sequences found using engineered Rescemu transposon				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 723 8221 Email: walbot@stanford.edu Plate: 1119066 row: B column: 12 Class: transposon-tagged. Location/Qualifiers				
FEATURES	1..89				
SOURCE	/organism="Zea mays" /mol_type="genomic DNA" /cultivar="mixed background W23/A188/B73/K55" /db_xref="taxon:4577" /taeue_type="leaf" /dev_stage="adult" /lab_host="DH10B" /clone_lib="1119 - Rescemu Grid AA" /note="Organ: leaf; Vector: Rescemu (engineered from pBuescript backbone); Site 1: BamHI; Site 2: BglII; Rescemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescemu, go to the web site 'www.zmdb.lastate.edu' and follow the links for 'Rescemu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."				
ORIGIN					
Query Match	75.3%;	Score 12.8;	DB 9;	Length 89;	
Best Local Similarity	56.2%;	Pred. No. 5.9e+04;			
Matches	9;	Conservative 5;	Mismatches 2;	Indels 0;	Gaps 0;
QY	2	CUGAUNUCAGUGCAGG 17			
DB	34	CTGATTCCTTGACAGG 49			
RESULT 19	AA948148/c	40 bp	mRNA	linear	EST 23-JUN-1998
LOCUS	AA948148/c				
DEFINITION	OM51104.81 NCI CGAP_C08 Homo sapiens cDNA clone IMAGE:1560223 3'				
ACCESSION	AA948148				
VERSION	AA948148.1	GI:3109401			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 40)				
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),				

JOURNAL  
COMMENT

Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Straubeberg, Ph.D.  
Email: cga@rs-remail.nih.gov  
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.  
Emmett-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
www.bio.linn.gov/dbp/image/image.html

FEATURES  
source

Trace considered overall poor quality  
Insert Length: 1052 Std Error: 0.00  
Seq primer: -40m13 fwd. RT from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

```
1.40
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1560223"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_C08"
/notes="Organ: Colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
colon adenocarcinoma, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."
```

## ORIGIN

Query Match 72.9%; Score 12.4; DB 1; Length 40;  
Best Local Similarity 50.0%; Pred. No. 8.6e+04;  
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCUGAUVUCAUUGC 14  
Db 40 CCGATTCAATTC 27

RESULT 20  
BZ594604/c 50 bp DNA linear GSS 07-JAN-2003  
LOCUS  
DEFINITION  
Arbidopsis thaliana genomic clone SALK\_084582.16.35.x, genomic  
survey sequence.

ACCESSION  
BZ594604  
KEYWORDS  
SOURCE  
ORGANISM  
Arbidopsis thaliana (chale crees)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis;  
1 (bases 1 to 50)

REFERENCE  
AUTHORS  
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
Gadgilab,C., Jeske,A., Karnes,M., Kim,C.D., Parker,H., Prednis,L.,  
Shim,P., Zimmerman,J., and Ecker,J.R.  
A Sequence-indexed library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)  
Contact: Joseph R. Ecker

JOURNAL  
COMMENT  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu

FEATURES  
source

This is single pass sequence recovered from the left border of  
TDNA. This sequence lies within an annotated intron of At3g44580.  
Class: TDNA tagged.  
Location/Qualifiers

```
1.50
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_084582.16.35.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at http://signal.salk.edu/cdna_protocols.html"
```

## ORIGIN

Query Match 72.9%; Score 12.4; DB 8; Length 50;  
Best Local Similarity 57.1%; Pred. No. 8.9e+04;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCUGAUVUCAUUGCA 15  
Db 35 CCGATTCAATTCGA 22

RESULT 21  
AA760149 54 bp mRNA linear EST 23-JAN-1998  
LOCUS  
DEFINITION  
vW70B11.r1 StrataGene mouse skin (#937313) Mus musculus cDNA clone  
IMAGE:1227741 5', mRNA sequence.

ACCESSION  
AA760149  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS  
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steplice,M., Tan,F., Underwood,K., Moore,B.,  
Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.

The WashU-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Maria M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.wustl.edu  
This clone is available royalty-free through LINL; contact the  
IMAGE Consortium (info@image.linn.gov) for further information.  
MGI:653333  
Seq primer: -28m13 rev1 RT from Amersham.

FEATURES  
source

```
1.54
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1227741"
/sex="females"
/tissue_type="whole skin"
/dev stage="11 weeks old"
/lab_host="SOLA (kanamycin resistant)"
/clone_lib="StrataGene mouse skin (#937313)"
/notes="Organ: skin; Vector: pBluescript SK-; Site 1:  
Bcor1; Site 2: XhoI; Cloned unidirectionally. Primer:
```



ACCESSION BH866175  
 VERSION BH866175.1 GI:22102073  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.  
 1 (bases 1 to 63)  
 REFERENCE Alonzo, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadriab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Becker, J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
 Unpublished (2001)  
 JOURNAL Contact: Joseph R. Becker  
 Salk Institute Genomic Analysis Laboratory (SIGAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left border of TDNA.  
 Class: TDNA tagged.  
 FEATURES Location/Qualifiers  
 1..63  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /ecotype="Col-0"  
 /db\_xref="taxon:3702"  
 /clone\_lib="SALK\_100839"  
 /note="PCR was performed on Arabidopsis thaliana T-DNA insertion lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"  
 ORIGIN  
 Query Match 72.9%; Score 12.4; DB 8; Length 63;  
 Best Local Similarity 50.0%; Pred. No. 9.2e+04;  
 Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 CUGAUUUCANUGCA 15  
 |||:||||:|  
 Db 28 CTGATTCATTGTA 15  
 RESULT 25  
 CR769964 65 bp DNA linear GSS 15-SEP-2004  
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-032E03-027723.  
 DEFINITION genomic survey sequence.  
 accession CR769964  
 version CR769964  
 keywords GSS.  
 source Arabidopsis thaliana (thale cress)  
 organism Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.  
 1 (bases 1 to 65)  
 REFERENCE Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weishaar, B.  
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana  
 Bioinformatics 19 (11), 1441-1442 (2003)  
 JOURNAL MEDLINE 22755829  
 PUBMED 12874060  
 REFERENCE 2 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and

TITLE Weishaar, B.  
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  
 JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
 MEDLINE 23117147  
 PUBMED 14756321  
 REFERENCE 3 Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weishaar, B.  
 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
 Biotechniques 35 (6), 1164-1168 (2003)  
 JOURNAL MEDLINE 23044198  
 PUBMED 14682050  
 REFERENCE 4 (bases 1 to 65)  
 JOURNAL Rosso, M.G., Li, Y., Strizhov, N. and Weishaar, B.  
 Direct Submission  
 Submitted (15-SEP-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene AT3G51880.  
 Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project.  
 GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.  
 FEATURES Location/Qualifiers  
 1..65  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone\_lib="GK-032E03-027723"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Col-0"  
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC106 (Genbank accession number: AY537513). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."  
 ORIGIN  
 Query Match 72.9%; Score 12.4; DB 9; Length 65;  
 Best Local Similarity 50.0%; Pred. No. 9.3e+04;  
 Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 CUGAUUUCANUGCA 15  
 |||:||||:|  
 Db 52 CTGATTCCTTCTGCA 39  
 RESULT 26  
 CG606249 65 bp mRNA linear GSS 02-OCT-2003  
 LOCUS OSTR283929 Mus musculus 129Sv/Ev Mus musculus cDNA clone OSTR283929.  
 DEFINITION mRNA sequence.  
 accession CG606249  
 version CG606249  
 keywords GSS.  
 source Mus musculus (house mouse)  
 organism Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 65)  
 REFERENCE Zambowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Pigott, J.J., Beltrande-Rio, H., Buxton, E.C., Edwards, J., Finch, R.A., Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jasing, C., Key, B.W., Li, K., Kipp, P., Kohlhauf, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,

TITLE Zhu,Q., Person,C. and Sands,A.T.  
wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
COMMENT Contact: Zambrowicz BP

OmniBank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: materials@lexgen.com  
Gene trap sequence tag generated by 3' RCE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)  
Classes: Gene trap.

#### FEATURES

source  
1..65  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone="OST283929"  
/cell\_type="embryonic stem cell"  
/clone\_lib="Mus musculus 129Sv/Ev"

#### ORIGIN

Query Match 72.9%; Score 12.4; DB 9; Length 65;  
Best Local Similarity 57.1%; Pred. No. 9.3e+04;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 3 UGAUUUUAUUGCAG 16  
:||||:|||||  
Db 8 TGATTCTACTGCAG 21

#### RESULT 27

AL853876 67 bp mRNA linear EST 02-DEC-2003  
AL853876 XGC-egg Xenopus tropicalis cDNA clone TEG9005021 3', mRNA sequence.

#### ACCESSION

AL853876 GI:38629511

#### VERSION

#### KEYWORDS

#### SOURCE

#### ORGANISM

Xenopus tropicalis (western clawed frog)

#### REFERENCE

1 (bases 1 to 67)  
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.  
Sanger Xenopus tropicalis EST project 2001 (11\_2003)

#### AUTHORS

#### JOURNAL

#### COMMENT

On Sep 15, 2002 this sequence version replaced gi:22874096.

Contact: Taylor R

Sanger Institute

Hinxton, Cambridgeshire, CB10 1SA, UK

Email: trop@sanger.ac.uk

Sanger Xenopus tropicalis EST project 2001

TROPICALIS\_SEQUENCE\_ID: TEG9005021.q1k17

Sequencing primer: 77

This sequence is from a Xenopus Gene Collection (XGC) library

constructed by Aaron M. Zorn.

cDNA was oligo dt primed from 5ug of poly A+ RNA from egg.

ECORI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the

5' end and NotI at the 3' end.

Vector: pCS107; Site 1: EcoRI; Site 2: NotI

Host: Escherichia coli XL1-blue.

#### FEATURES

#### SOURCE

1..67  
/organism="Xenopus tropicalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8364"  
/clone="TEG9005021"  
/dev\_stage="egg"  
/lab\_host="Escherichia coli XL1-blue"  
/clone\_lib="XGC-egg"

/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dt primed from 5ug of poly A+ RNA from egg.  
ECORI-NotI cut cDNA was then ligated into pCS107 with  
EcoRI at the 5' end and NotI at the 3' end"

#### ORIGIN

Query Match 72.9%; Score 12.4; DB 1; Length 67;  
Best Local Similarity 57.1%; Pred. No. 9.3e+04;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 2 CUGAUUUAUUGCA 15  
:||||:|||||  
Db 41 CTGATTGCAATGCA 54

#### RESULT 28

BM514574/c 74 bp mRNA linear EST 15-FEB-2002  
LOCUS ky05b03.y1 Parastrongyloides trichosuri PA SL1 TOPO v1 Murphy  
DEFINITION Chlapelli McCarter Parastrongyloides trichosuri cDNA 5', mRNA  
sequence.

#### ACCESSION

BM514574 GI:18685717

#### VERSION

#### KEYWORDS

#### SOURCE

#### ORGANISM

#### REFERENCE

1 (bases 1 to 74)  
McCarter,J., Clifton,S., Chlapelli,B., Pape,D., Martin,J.,  
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,  
Tsagarisshvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
Underwood,K., Stepien,M., Allen,M., Person,B., Swaller,T.,  
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
McCann,R., Waterston,R. and Wilson,R.

#### AUTHORS

#### COMMENT

The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)  
Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington Univ. Nematode EST Project, 1999  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

#### JOURNAL

#### COMMENT

Nematodes provided by Dr. Warwick Grant of AgResearch, New Zealand  
(warwick.grant@agresearch.co.nz). The library was constructed by  
Brandi Chlapelli and Dr. James McCarter (bchlapell@watson.wustl.edu  
and jmcarter@watson.wustl.edu) at Washington University, St. Louis.  
DNA Sequencing by: Washington University Genome Sequencing Center  
St. Louis

#### REFERENCE

Seq primer: SL1 primer.

#### AUTHORS

#### JOURNAL

#### COMMENT

Location/Qualifiers

#### FEATURES

#### SOURCE

1..74  
/organism="Parastrongyloides trichosuri"  
/mol\_type="mRNA"  
/db\_xref="taxon:131310"  
/dev\_stage="Parasitic adults"  
/lab\_host="MDH10B"  
/clone\_lib="Parastrongyloides trichosuri PA SL1 TOPO v1  
Murphy Chlapelli McCarter"  
/note="Vector: pCRII-TOPO (Invitrogen); Site 1: EcoRI; The  
library was constructed by Claire Murphy, Brandi  
Chlapelli, and Dr. James McCarter at Washington  
University, St. Louis. Oligo(dt)-SL1 PCR based library.  
Parastrongyloides trichosuri parasitic adult cDNA PCR  
products of size >400 nucleotides containing SL1 on the 5'  
end and oligo(dt) on the 3' end were non-directionally  
cloned into pCRII-TOPO(Invitrogen) following the TOPO TA  
cloning protocol. Nematodes were provided by Dr. Warwick  
Grant of AgResearch, New Zealand  
(warwick.grant@agresearch.co.nz). Worms were harvested  
from Australian brush-tailed possum (Trichosuri vulpecula)

and washed thoroughly to remove host contamination. Note that despite this effort, host contamination of the library is possible."

## ORIGIN

Query Match 72.9%; Score 12.4; DB 4; Length 74;  
Best Local Similarity 50.0%; Pred. No. 9.4e+04;  
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
QY 2 CUGAUNUCAUUGCA 15  
Db 25 CTGATTCATTCCTCA 12

## RESULT 29

## LOCUS

AZ468373 74 bp DNA linear GSS 04-OCT-2000

DEFINITION 1M0281A22F Mouse 10kb plasmid UGCCIM library Mus musculus genomic

clone UGCCIM0281A22 F, genomic survey sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

## COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0281 row: A column: 22  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 74.  
Location/Qualifiers

## FEATURES

## source

1. 74  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCCIM0281A22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42n; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF128072.1), a copy-number  
inducible derivative of plasmid RI. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to

adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

Query Match 72.9%; Score 12.4; DB 8; Length 74;  
Best Local Similarity 50.0%; Pred. No. 9.4e+04;  
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCUGAUNUCAUUGC 14  
Db 23 CCGATTCATTCCTC 10

## RESULT 30

## LOCUS

BZ593321 77 bp DNA linear GSS 07-JAN-2003

DEFINITION SALK\_070016.16.25 x Arabidopsis thaliana TDNA insertion lines

Arabidopsis thaliana genomic clone SALK\_070016.16.25.x, genomic  
survey sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
Gadriab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
Shim, P., Zimmerman, J. and Ecker, J.R.  
A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.  
Location/Qualifiers

## JOURNAL

## COMMENT

1. 77  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone="SALK\_070016.16.25.x"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at http://signal.salk.edu/tdna\_protocols.html"

## FEATURES

## source

1. 77  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone="SALK\_070016.16.25.x"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at http://signal.salk.edu/tdna\_protocols.html"

## ORIGIN

Query Match 72.9%; Score 12.4; DB 8; Length 77;  
Best Local Similarity 50.0%; Pred. No. 9.5e+04;  
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
QY 2 CUGAUNUCAUUGCA 15  
Db 57 CTGATTCATTCCTCA 70

## RESULT 31

## LOCUS

AW672652 79 bp mRNA linear EST 26-SEP-2001



REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 81)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0070 row: M column: 06  
Seq primer: CACACGAAACAGCATGACC  
Class: plasmid ends  
High quality sequence stop: 81.

FEATURES  
source

1. 81  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG1M0070M06"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 72.9%; Score 12.4; DB 8; Length 81;  
Best Local Similarity 50.0%; Pred. No. 9.6e+04;  
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCUGAUTCATGCG 14  
||:||||:||||  
DB 73 CTTGATTCATGCG 60

RESULT 34  
LOCUS BZ587139/c 82 bp DNA linear GSS 17-DEC-2002  
DEFINITION 3590\_1\_10\_1\_C02\_2EL\_x\_1\_3590 - RescuedMu Grid M Zea mays genomic.  
ACCESSION BZ587139  
VERSION BZ587139.1 GI:27222200  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

## REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 82)  
Walbot, V.  
Maize genomic sequences found using engineered RescuedMu transposon  
Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu

JOURNAL  
COMMENT

Possible ligation site of ends cut by 2 different endonucleases.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 3590\_1\_10\_1 column: 11  
Class: transposon-tagged.

FEATURES  
source

1. 82  
Location/Qualifiers  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/Al88/B73/K55"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_id="3590 - RescuedMu Grid M"  
/note="Organ: leaf; Vector: RescuedMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescuedMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescuedMu, go to the web site 'www.emdb.iastate.edu' and follow the links for 'RescuedMu'. Grid M was grown at University of Arizona in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmid. DH10B cells were transformed and then screened on LB plates with ampicillin."

## ORIGIN

Query Match 72.9%; Score 12.4; DB 8; Length 82;  
Best Local Similarity 50.0%; Pred. No. 9.6e+04;  
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCUGAUTCATGCG 14  
||:||||:||||  
DB 57 CTTGATTCATGCG 44

RESULT 35  
LOCUS CN855612/c 83 bp mRNA linear EST 03-JUN-2004  
DEFINITION 000721AA002844HT (AAA) Royal Gala 59 DAFI fruit, seeds removed  
ACCESSION CN855612  
VERSION CN855612.1 GI:48110989  
KEYWORDS EST.  
SOURCE Malus x domestica (cultivated apple)  
ORGANISM Malus x domestica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid1; Rosales; Rosaceae; Maloideae; Malus. 1 (bases 1 to 83)  
Benning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B., McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.

HorResearch Apple EST Project  
Unpublished (2004)  
Contact: Gleave, A.  
Sequencing Facility  
The Horticulture and Food Research Institute of New Zealand Ltd  
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand

Tel: 00 64 09 815 4200  
 Fax: 00 64 09 815 4201  
 Email: es@hortresearch.co.nz.  
 Location/Qualifiers

# FEATURES

source

1..83  
 /organism="Malus x domestica"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3750"  
 /clone="AAA002844"  
 /issue\_type="fruit"  
 /dev\_stage="59 days after full bloom, seeds removed"  
 /clone\_1ib="(AAAA) Royal Gala 59 DAFB fruit, seeds removed"  
 /note="Vector: PBK-CMV; library sequenced by Genesis Research & Development"

# ORIGIN

Query Match 72.9%; Score 12.4; DB 7; Length 83;  
 Best Local Similarity 50.0%; Pred. No. 9.6e+04;  
 Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 3 UGAUUCAUUGCAG 16  
 :|::||::|||  
 14 TGCTTCATTGCAG 1

RESULT 36 BH791384 83 bp DNA linear GSS 02-APR-2002  
 LOCUS SALK\_059855.54.50.x Arabidopsis thaliana TDNA insertion lines  
 DEFINITION Arabidopsis thaliana genomic clone SALK\_059855.54.50.x, genomic survey sequence.

ACCESSION BH791384.1 GI:19885192  
 VERSION BH791384  
 KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 83)

REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gatinho,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shum,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL Unpublished (2001)  
 COMMENT Contact: Joseph R. Ecker

SALT Institute Genomic Analysis Laboratory (SIGAL)

The Salt Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379

Email: eckers@salt.edu

FEATURES This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At5g44580. Class: TDNA tagged.

Location/Qualifiers

1..83  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /ecotype="Col-0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_059855.54.50.x"  
 /clone\_1ib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/cdna\\_protocol.html](http://signal.salk.edu/cdna_protocol.html)"

ORIGIN

Query Match 72.9%; Score 12.4; DB 8; Length 83;  
 Best Local Similarity 57.1%; Pred. No. 9.6e+04;  
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 2 UGAUUCAUUGCA 15  
 :|::||::|||  
 42 CCGATTTCATTGCA 29

# RESULT 37

AZ820505 91 bp DNA linear GSS 20-FEB-2001  
 LOCUS 2M0092P06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0092P06 R, genomic survey sequence.

ACCESSION AZ820505  
 VERSION AZ820505.1 GI:12990329  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 91)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss

University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0092 row: P column: 06

Seq primer: CACACAGGAACACGATATGACC

Class: plasmid ends

FEATURES High quality sequence stop: 91.  
 Location/Qualifiers

1..91  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0092P06"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gii473211|gb|AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 72.9%; Score 12.4; DB 8; Length 91;  
 Best Local Similarity 57.1%; Pred. No. 9.7e+04;  
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAUUCANUCGACG 17  
 ||:||||:||||  
 DB 23 GATTTCATTACGAG 36

RESULT 38  
 C00319/c 96 bp mRNA linear EST 31-DEC-2002  
 LOCUS HUMG0006024 Human adult (K.Okubo) Homo sapiens cDNA, mRNA  
 DEFINITION sequence.  
 ACCESSION C00319  
 VERSION C00319.1 GI:1432549  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 96)  
 Okubo, K.  
 BodyMap; human gene expression database  
 Unpublished (1995)  
 CONTACT: Okubo, K.  
 Institute for Molecular and Cellular Biol  
 Osaka University  
 1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan  
 Tel: 06-877-5111 (ex.3315)  
 Email: koueak@imcb.osaka-u.ac.jp  
 We are not submitting the same cDNA sequence redundantly to DBJ  
 since 1993. For the abundance information of clones with this  
 sequence in this library and as well as in other 3'-directed  
 libraries, see: <http://www.imcb.osaka-u.ac.jp/bodymap>. The  
 sequences of the clones represented by this GS sequences is also  
 found there.

FEATURES  
 source Location/Qualifiers  
 1..96  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="adult"  
 /clone\_lib="Human adult (K.Okubo)"  
 /note="One or more human adult tissue"

ORIGIN  
 Query Match 72.9%; Score 12.4; DB 6; Length 96;  
 Best Local Similarity 50.0%; Pred. No. 9.8e+04;  
 Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCUGANUUCANUCC 14  
 ||:||||:||||  
 DB 47 CCTGATTTCATTCC 34

RESULT 39  
 CV296295/c 96 bp mRNA linear EST 23-SEP-2004  
 LOCUS EST84672 petunia floral development cDNA library Petunia x hybrida  
 DEFINITION cDNA clone Petunia-DeVA-12-E07 5' end, mRNA sequence.  
 ACCESSION CV296295  
 VERSION CV296295.1 GI:52587436  
 KEYWORDS EST.  
 SOURCE Petunia x hybrida  
 ORGANISM Petunia x hybrida  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamids; Solanales; Solanaceae; Petunia.  
 1 (bases 1 to 96)  
 Shibuya, K., Underwood, B., Loucas, H., Farmerie, W., Jones, M. and  
 Clark, D.  
 Petunia x hybrida EST collection

JOURNAL  
 COMMENT Unpublished (2004)  
 Contact: David Clark  
 UF Floriculture Biotechnology Lab  
 University of Florida  
 Environmental Horticulture Department, 1545 Piffeld Hall, Box  
 110670, Gainesville, FL 32611-0670, USA  
 Tel: 352-392-1831 x370  
 Fax: 352-392-3870  
 Email: dclark@mail.ufl.edu  
 Contact Dr. Clark (dclark@mail.ufl.edu) for clone information  
 Seq primer: 73 primer.

FEATURES  
 source Location/Qualifiers  
 1..96  
 /organism="Petunia x hybrida"  
 /mol\_type="mRNA"  
 /cultivar="Mitchell Diploid (aka. Mitchell, aka W15 in  
 Europe)"  
 /db\_xref="taxon:4102"  
 /clone="petunia-DeVA-12-E07"  
 /tissue\_type="all floral organs"  
 /lab\_host="lambda ZAPII unidirectional"  
 /clone\_lib="petunia floral development cDNA library"  
 /note="Vector: pBluescript SK-; Site 1, EcoRI; Site 2:  
 XhoI; supplier: Petunia x hybrida cv. Mitchell Diploid  
 plants were grown from seeds to a fully flowering stage  
 under standard greenhouse conditions. Ten entire flowers  
 of six developmental stages were collected on the same day  
 from plants grown in standard greenhouses. The flower  
 stages were as follows in chronological order from  
 youngest to oldest: stage 1 - no color in corolla; corolla  
 0.5 inches long stage 2 - first sign of color in corolla;  
 corolla .75-1 inches long stage 3 - fully elongated  
 corolla (not open); corolla 1.5 inches long stage 4 -  
 fully open corolla; anthers not yet dehiscent stage 5 -  
 fully open corolla; freshly anthesed, bright yellow  
 corolla; wet stigma stage 6 - pre-anthesed; yellowing of  
 corolla tube; dry brown pollen (if present); stigma dry.  
 Total RNA was extracted from each sample, and 100  
 micrograms of each sample was combined for subsequent poly  
 A+ mRNA selection and cDNA synthesis."

ORIGIN  
 Query Match 72.9%; Score 12.4; DB 7; Length 96;  
 Best Local Similarity 50.0%; Pred. No. 9.8e+04;  
 Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 CUGANUUCANUGCA 15  
 ||:||||:||||  
 DB 84 CTGATTTCATTGTA 71

RESULT 40  
 BI090229/c 98 bp mRNA linear EST 20-JUN-2001  
 LOCUS 602857182P1 NIH\_MGC\_10 Homo sapiens cDNA clone IMAGE:498476 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BI090229  
 VERSION BI090229.1 GI:14508559  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 98)  
 NIH-MGC <http://mgc.ncl.nih.gov/>,  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cga@bcr-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: Incyte Genomics, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: L1AM11027 row: c column: 21

High quality sequence stop: 98.

Location/Qualifiers

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Source  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4998476"  
/cell\_line="MGC36"  
/lab\_host="DH10B"  
/clone\_id="NH\_MGC\_10"  
/note="Organ: cervix; Vector: PCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.5 Kb. Library prepared by Life  
Technologies."

## ORIGIN

Query Match 72.9%; Score 12.4; DB 4; Length 98;

Best Local Similarity 50.0%; Pred. No. 9.9e+04;

Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTGAUUDCAUUGC 14  
||:||||:|  
Db 31 CCTGATTCATTC 18

Search completed: May 13, 2005, 17:50:53  
Job time : 845.127 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2005, 16:49:04 ; Search time 1090.95 Seconds  
(without alignments)  
1687.800 Million cell updates/sec

Title: US-09-927-046-2332

Perfect score: 38  
Sequence: 1 ccgcaucgagcgagcgccgcuuagcgcaaaaacagc 38

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 2238514

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :  
1: gb\_da:\*  
2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_scs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	38	6	AX580494 Sequence
2	36	94.7	37	6	AX583594 Sequence
3	31.8	83.7	38	6	AX218695 Sequence
4	31.4	82.6	38	6	AX218695 Sequence
5	31.4	82.6	38	6	AX218695 Sequence
6	31.4	82.6	38	6	AX218695 Sequence
7	31.2	82.1	38	6	AX311496 Sequence
8	30.8	82.1	38	6	AX311496 Sequence
9	30.8	81.1	38	6	AX330070 Sequence
10	30.8	81.1	38	6	AX330070 Sequence
11	30.6	80.5	38	6	AX332172 Sequence
12	30.4	80.0	38	6	AX332172 Sequence
13	30.4	80.0	38	6	AX332172 Sequence
14	30.4	80.0	38	6	AX332172 Sequence
15	30.4	80.0	38	6	AX332172 Sequence
16	30.4	80.0	38	6	AX332172 Sequence
17	30.2	79.5	38	6	AX330741 Sequence
18	30.2	79.5	38	6	AX330741 Sequence
19	30	78.9	38	6	AX330124 Sequence

20	30	78.9	38	6	AR330364 Sequence
21	30	78.9	38	6	AR332137 Sequence
22	30	78.9	38	6	AX227896 Sequence
23	30	78.9	38	6	AX580822 Sequence
24	29.8	78.4	38	6	AR330838 Sequence
25	29.8	78.4	38	6	AR330943 Sequence
26	29.8	78.4	38	6	AR331128 Sequence
27	29.8	78.4	38	6	AX218680 Sequence
28	29.8	78.4	38	6	AX218680 Sequence
29	29.8	78.4	38	6	AX218680 Sequence
30	29.8	78.4	38	6	AX222419 Sequence
31	29.6	77.9	38	6	AR332151 Sequence
32	29.6	77.9	38	6	AX218714 Sequence
33	29.6	77.9	38	6	AX218673 Sequence
34	29.6	77.9	38	6	AX219601 Sequence
35	29.6	77.9	38	6	AX222613 Sequence
36	29.6	77.9	38	6	AX227899 Sequence
37	29.6	77.9	38	6	AX580764 Sequence
38	29.6	77.9	38	6	AX580873 Sequence
39	29.4	77.4	38	6	AR330254 Sequence
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41	29.4	77.4	38	6	AR331020 Sequence
42	29.4	77.4	38	6	AR331551 Sequence
43	29.4	77.4	38	6	AR332105 Sequence
44	29.4	77.4	38	6	AR332157 Sequence
45	29.4	77.4	38	6	AR333898 Sequence
46	29.4	77.4	38	6	AX219574 Sequence
47	29.4	77.4	38	6	AX423799 Sequence
48	29.4	77.4	38	6	AX581103 Sequence
49	29.2	76.8	38	6	AR046561 Sequence
50	29.2	76.8	38	6	154013 Sequence 17
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56	29.2	76.8	38	6	AX218962 Sequence
57	29.2	76.8	38	6	AX219605 Sequence
58	29.2	76.8	38	6	AX222374 Sequence
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61	29.2	76.8	38	6	AX228365 Sequence
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64	29	76.3	38	6	AR335862 Sequence
65	29	76.3	38	6	AX218598 Sequence
66	29	76.3	38	6	AX218781 Sequence
67	29	76.3	38	6	AX218967 Sequence
68	29	76.3	38	6	AX423865 Sequence
69	29	76.3	38	6	AX424179 Sequence
70	29	76.3	38	6	AX580589 Sequence
71	28.8	75.8	38	6	AR330131 Sequence
72	28.8	75.8	38	6	AR330645 Sequence
73	28.8	75.8	38	6	AR330926 Sequence
74	28.8	75.8	38	6	AR332998 Sequence
75	28.8	75.8	38	6	AR333246 Sequence
76	28.8	75.8	38	6	AR333642 Sequence
77	28.8	75.8	38	6	AR334821 Sequence
78	28.8	75.8	38	6	AR335093 Sequence
79	28.8	75.8	38	6	AR336492 Sequence
80	28.8	75.8	38	6	AX218596 Sequence
81	28.8	75.8	38	6	AX218612 Sequence
82	28.8	75.8	38	6	AX218613 Sequence
83	28.8	75.8	38	6	AX218829 Sequence
84	28.8	75.8	38	6	AX218872 Sequence
85	28.8	75.8	38	6	AX222333 Sequence
86	28.8	75.8	38	6	AX227877 Sequence
87	28.8	75.8	38	6	AX228151 Sequence
88	28.8	75.8	38	6	AX228186 Sequence
89	28.8	75.8	38	6	AX423978 Sequence
90	28.8	75.8	38	6	AX580357 Sequence
91	28.8	75.8	38	6	AX580573 Sequence
92	28.6	75.3	38	6	AR330224 Sequence

93 28.6 75.3 38 6 AR330756 Sequence  
94 28.6 75.3 38 6 AR330934 Sequence  
95 28.6 75.3 38 6 AR331361 Sequence  
96 28.6 75.3 38 6 AR331857 Sequence  
97 28.6 75.3 38 6 AR331852 Sequence  
98 28.6 75.3 38 6 AX222647 Sequence  
99 28.6 75.3 38 6 AX222769 Sequence  
100 28.6 75.3 38 6 AX222850 Sequence

## ALIGNMENTS

RESULT 1  
AX580494 38 bp RNA linear PAT 10-JAN-2003  
LOCUS Sequence 2332 from Patent WO0211674.  
ACCESSION AX580494  
VERSION AX580494.1 GI:27649696  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE other sequences; artificial sequences.  
AUTHORS 1 Thompson,J., Mcswigen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.  
and Grube,A.  
TITLE Method and reagent for the inhibition of calcium activated chloride  
channel-1 (Clca-1)  
JOURNAL Patent: WO 0211674-A 2332 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;  
Thompson, James (US)  
LOCATION/Qualifiers  
FEATURES 1. .38  
source /organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"  
ORIGIN  
Query Match 100.0%; Score 38; DB 6; Length 38;  
Best Local Similarity 81.6%; Pred. No. 1.7e-05;  
Matches 31; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCUGCAUCGAGGCGGUAAGCGCGGAAAAUACAG 38  
Db 1 CCTGCAATCTGATGAGCGCGTTAGCGCGGAAAAATCAG 38  
RESULT 2  
AX583594 37 bp RNA linear PAT 10-JAN-2003  
LOCUS Sequence 5432 from Patent WO0211674.  
ACCESSION AX583594  
VERSION AX583594.1 GI:27655404  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE other sequences; artificial sequences.  
AUTHORS 1 Thompson,J., Mcswigen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.  
and Grube,A.  
TITLE Method and reagent for the inhibition of calcium activated chloride  
channel-1 (Clca-1)  
JOURNAL Patent: WO 0211674-A 5432 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;  
Thompson, James (US)  
LOCATION/Qualifiers  
FEATURES 1. .37  
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/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
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misc\_feature 1. .8  
misc\_feature 1. .8

misc\_feature /note="2'-O-Methyl"  
misc\_feature 1. .4  
/note="Phosphorothioate 3'-internucleotide linkage"  
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/note="2'-deoxy-2'-C-Allyl"  
misc\_feature 12  
/note="2'-O-Methyl"  
misc\_feature 14. .26  
/note="2'-O-Methyl"  
misc\_feature 28. .29  
/note="2'-O-Methyl"  
misc\_feature 31. .36  
/note="2'-O-Methyl"  
misc\_feature 37  
/note="n strands for inverted deoxyabasic derivative"  
ORIGIN  
Query Match 94.7%; Score 36; DB 6; Length 37;  
Best Local Similarity 80.6%; Pred. No. 0.00013;  
Matches 29; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 CCUGCAUCGAGGCGGUAAGCGCGGAAAAUACAG 37  
Db 1 CTGCAATCTGATGAGCGCGTTAGCGCGGAAAAATCAG 36  
RESULT 3  
AX218695 38 bp RNA linear PAT 07-SEP-2001  
LOCUS Sequence 4137 from Patent WO0159103.  
ACCESSION AX218695  
VERSION AX218695.1 GI:15546419  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE other sequences; artificial sequences.  
AUTHORS 1 Blatt,L., Mcswigen,J. and Chowrira,B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL Patent: WO 0159103-A 4137 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
Mcswigen, James (US) ; Chowrira, Bharat M. (US)  
LOCATION/Qualifiers  
FEATURES 1. .38  
source /organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"  
ORIGIN  
Query Match 83.7%; Score 31.8; DB 6; Length 38;  
Best Local Similarity 74.3%; Pred. No. 0.0087;  
Matches 26; Conservative 7; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 CCUGCAUCGAGGCGGUAAGCGCGGAAAAUACAG 36  
Db 2 CTTTAATCTGATGAGCGCGTTAGCGCGGAAAAATCA 36  
RESULT 4  
AX218894 38 bp RNA linear PAT 07-SEP-2001  
LOCUS Sequence 4336 from Patent WO0159103.  
ACCESSION AX218894  
VERSION AX218894.1 GI:15546618  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE other sequences; artificial sequences.  
AUTHORS 1 Blatt,L., Mcswigen,J. and Chowrira,B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and



Dbl	1	CCCCGAAACTGATGAGCGCCGTTAGGCCCAAAAAGTCA	36
RESULT 9			
LOCUS	AR330070	38 bp	RNA
DEFINITION	Sequence 7472 from patent US 6566127.		linear
ACCESSION	AR330070		PAT 17-AUG-2003
VERSION	AR330070.1		
KEYWORDS			
SOURCE			
ORGANISM	Unknown.		
REFERENCE	Unclassified. 1 (bases 1 to 38)		
AUTHORS	Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.		
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 7472 20-MAY-2003;		
JOURNAL	Location/Qualifiers		
FEATURES	1..38		
source	/organism="unknown" /mol_type="unassigned RNA"		
ORIGIN			
Query Match	81.1%; Score 30.8; DB 6;	Length 38;	
Best Local Similarity	76.5%; Pred.No.0.024;		
Matches	26; Conservative 6; Mismatches 2; Indels 0; Gaps 0;		
OY	2 CUCGAUUCUGAUGAGCGCGUTDAGCCGCAAAAAAUC 35		
Dbl	2 CGCAGCTGTGATGAGCGCGTTAGGCCGAAAAATC 35		
RESULT 10			
LOCUS	AR331271	38 bp	RNA
DEFINITION	Sequence 8673 from patent US 6566127.		linear
ACCESSION	AR331271		PAT 17-AUG-2003
VERSION	AR331271.1		
KEYWORDS	GI:33717079		
SOURCE			
ORGANISM	Unknown.		
REFERENCE	Unclassified. 1 (bases 1 to 38)		
AUTHORS	Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.		
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 8673 20-MAY-2003;		
JOURNAL	Location/Qualifiers		
FEATURES	1..38		
source	/organism="unknown" /mol_type="unassigned RNA"		
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Query Match	81.1%; Score 30.8; DB 6;	Length 38;	
Best Local Similarity	76.5%; Pred.No.0.024;		
Matches	26; Conservative 6; Mismatches 2; Indels 0; Gaps 0;		
OY	1 CCUGCAAUCUGAUGAGCGCGUAGGCCGAAANAUA 34		
Dbl	1 CCTGCAGCTGATGAGCGCGTTAGGCCGAAANAATT 34		
RESULT 11			
LOCUS	AR332172	38 bp	RNA
DEFINITION	Sequence 9574 from patent US 6566127.		linear
ACCESSION	AR332172		PAT 17-AUG-2003
VERSION	AR332172.1		
KEYWORDS	GI:33717980		
SOURCE			
ORGANISM	Unknown.		
REFERENCE	Unclassified.		

[illegible]





QY 1 CCUGCAUUCGAGGCCGCGUAGCCGCGAANAUCAG 38  
DB 1 CCTGCCATCTGATGAGCCGCTTAGGCCGAAAGTTGATG 38

RESULT 23  
LOCUS AX580822 38 bp RNA linear PAT 10-JAN-2003  
DEFINITION Sequence 2660 from Patent WO211674.  
ACCESSION AX580822  
VERSION AX580822.1 GI:27650024  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 other sequences; artificial sequences.  
AUTHORS Thompson, J., McSwiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.  
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)  
JOURNAL Patent: WO 0211674-A 2660 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)  
FEATURES Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"

ORIGIN  
Query Match 78.4%; Score 29.8; DB 6; Length 38;  
Best Local Similarity 75.8%; Pred. No. 0.065;  
Matches 25; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCAUUCGAGGCCGCGUAGCCGCGAANA 33  
DB 4 GCAATCTGATGAGCCGCTTAGGCCGAAANA 33

RESULT 24  
LOCUS AR330838 38 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 8240 from patent US 6566127.  
ACCESSION AR330838  
VERSION AR330838.1 GI:33716646  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 Unclassified.  
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Bacabedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 8240 20-MAY-2003;  
JOURNAL Location/Qualifiers  
1..38  
/organism="unknown"  
/mol\_type="unassigned RNA"

ORIGIN  
Query Match 78.4%; Score 29.8; DB 6; Length 38;  
Best Local Similarity 75.8%; Pred. No. 0.065;  
Matches 25; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 6 AAUCUGAGGCCGCGUAGCCGCGAANAUCAG 38  
DB 6 ATTCTGATGAGCCGCTTAGGCCGAAANAATCAAG 38

RESULT 25  
LOCUS AR330943 38 bp RNA linear PAT 17-AUG-2003

DEFINITION Sequence 8345 from patent US 6566127.  
ACCESSION AR330943  
VERSION AR330943.1 GI:33716751  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 Unclassified.  
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Bacabedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 8345 20-MAY-2003;  
JOURNAL Location/Qualifiers  
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ORIGIN  
Query Match 78.4%; Score 29.8; DB 6; Length 38;  
Best Local Similarity 75.8%; Pred. No. 0.065;  
Matches 25; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 6 AAUCUGAGGCCGCGUAGCCGCGAANAUCAG 38  
DB 6 ATTCTGATGAGCCGCTTAGGCCGAAANAATCAAG 38

RESULT 26  
LOCUS AR331128 38 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 8530 from patent US 6566127.  
ACCESSION AR331128  
VERSION AR331128.1 GI:33716936  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 Unclassified.  
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Bacabedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 8530 20-MAY-2003;  
JOURNAL Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned RNA"

ORIGIN  
Query Match 78.4%; Score 29.8; DB 6; Length 38;  
Best Local Similarity 72.7%; Pred. No. 0.065;  
Matches 24; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 CUGCAUUCGAGGCCGCGUAGCCGCGAANA 34  
DB 2 CTGAATCTGATGAGCCGCTTAGGCCGAAAT 34

RESULT 27  
LOCUS AX218680 38 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 4122 from Patent WO0159103.  
ACCESSION AX218680  
VERSION AX218680.1 GI:15546404  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 other sequences; artificial sequences.  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of c220 and nogo gene expression Patent: WO 0159103-A 4122 16-AUG-2001;  
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;





LOCUS	AX227899	38 bp	RNA	linear	PAT 10-SEP-2003
DEFINITION	Sequence 1271 from Patent WO0157206.				
ACCESSION	AX227899				
VERSION	AX227899.1	GI:15557040			
KEYWORDS					
SOURCE					
ORGANISM	synthetic construct				
REFERENCE	synthetic construct				
AUTHORS	other sequences; artificial sequences.				
TITLE	1				
JOURNAL	Fattaey, A.R., Jarvis, T., Mcswiggen, J., Booher, R.N. and Holman, P.S.				
FEATURES	Method and reagent for the inhibition of checkpoint kinase-1 (chk				
source	1 enzyme				
ORIGIN	Patent: WO 0157206-A 1271 09-AUG-2001;				
	RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)				
	Location/Qualifiers				
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	/organism="synthetic construct"				
	/mol_type="unassigned RNA"				
	/db_xref="taxon:32630"				
Query Match	77.9%; Score 29.6; DB 6;	Length 38;			
Best Local Similarity	75.0%; Pred. No. 0.08;				
Matches	27; Conservative 5; Mismatches 4; Indels 0; Gaps 0;				
QY	1 CCUGCAUCUGAGGCGCCGUAAGCCGAAAUAUCA 36				
Db	1 CATGCAGACTGATGAGCGCGTTAGGCCGAAAACCA 36				
RESULT 37					
LOCUS	AX580764	38 bp	RNA	linear	PAT 10-JAN-2003
DEFINITION	Sequence 2602 from Patent WO0211674.				
ACCESSION	AX580764				
VERSION	AX580764.1	GI:27649966			
KEYWORDS					
SOURCE					
ORGANISM	synthetic construct				
REFERENCE	synthetic construct				
AUTHORS	other sequences; artificial sequences.				
TITLE	1				
JOURNAL	Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.				
FEATURES	and Grube, A.				
source	Method and reagent for the inhibition of calcium activated chloride				
	channel-1 (clca-1)				
	Patent: WO 0211674-A 2602 14-FEB-2002;				
	RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;				
	Thompson, James (US)				
	Location/Qualifiers				
	1..38				
	/organism="synthetic construct"				
	/mol_type="unassigned RNA"				
	/db_xref="taxon:32630"				
	/note="Enzymatic Nucleic Acid"				
ORIGIN					
Query Match	77.9%; Score 29.6; DB 6;	Length 38;			
Best Local Similarity	72.2%; Pred. No. 0.08;				
Matches	26; Conservative 6; Mismatches 4; Indels 0; Gaps 0;				
QY	3 UGCAUCUGAUGAGCGCCGUAAGCCGAAAUAUCA 38				
Db	3 TGGGAACCTGATGAGCGCGTTAGGCCGAAAAGATCAG 38				
RESULT 38					
LOCUS	AX580873	38 bp	RNA	linear	PAT 10-JAN-2003
DEFINITION	Sequence 2711 from Patent WO0211674.				
ACCESSION	AX580873				
VERSION	AX580873.1	GI:27650075			
KEYWORDS					
SOURCE	synthetic construct				

ORGANISM	synthetic construct	other sequences; artificial sequences.
REFERENCE	1	Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D. E.
AUTHORS		and Grube, A.
TITLE		Method and reagent for the inhibition of calcium activated chloride
JOURNAL		channel-1 (cica-1)
		Patent: WO 0211674-A 2711 14-FEB-2002;
		RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
		Thompson, James (US)
FEATURES		Location/Qualifiers
source	1..38	
	/organism="synthetic construct"	
	/mol_type="unassigned RNA"	
	/db_xref="taxon:32630"	
	/note="Enzymatic Nucleic Acid"	
ORIGIN		
Query Match	77.9%; Score 29.6; DB 6; Length 38;	
Best Local Similarity	72.2%; Pred. No. 0.08; Mismatches 26; Conservative 6; Indels 4; Gaps 0;	
Matches		
Oy	2 CUGCAUCUGAGGCGGUAAGGCGGAAAAAUCAG 37	
	2 CTGACACTGATGAGCGCGTTAGGCGGAAATTCAG 37	
Db		
RESULT 39		
AR330254	38 bp RNA	linear PAT 17-AUG-2003
LOCUS		
DEFINITION	Sequence 7656 from patent US 6566127.	
ACCESSION	AR330254	
VERSION	AR330254.1	GI:33716062
KEYWORDS		
SOURCE		
ORGANISM	Unknown.	
REFERENCE	Unknown.	
AUTHORS	Unclassified.	
TITLE	1 (bases 1 to 38)	
JOURNAL	Pavco, P., Mcswiggen, J. A., Stinchcomb, D. T. and Escobedo, J.	
FEATURES	Method and reagent for the treatment of diseases or conditions	
source	related to levels of vascular endothelial growth factor receptor	
	Patent: US 6566127-A 7656 20-MAY-2003;	
	Location/Qualifiers	
	1..38	
	/organism="unknown"	
	/mol_type="unassigned RNA"	
ORIGIN		
Query Match	77.4%; Score 29.4; DB 6; Length 38;	
Best Local Similarity	80.6%; Pred. No. 0.098; Mismatches 25; Conservative 5; Indels 1; Gaps 0;	
Matches		
Oy	7 AUCUGAGGAGCGGUAAGGCGGAAAAAUCAG 37	
	7 AACTGATGAGGAGCGGTTAGGCGGAAAAATCAG 37	
Db		
RESULT 40		
AR330461	38 bp RNA	linear PAT 17-AUG-2003
LOCUS		
DEFINITION	Sequence 7863 from patent US 6566127.	
ACCESSION	AR330461	
VERSION	AR330461.1	GI:33716269
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 38)	
TITLE	Pavco, P., Mcswiggen, J. A., Stinchcomb, D. T. and Escobedo, J.	
JOURNAL	Method and reagent for the treatment of diseases or conditions	
FEATURES	related to levels of vascular endothelial growth factor receptor	
source	Patent: US 6566127-A 7863 20-MAY-2003;	
	Location/Qualifiers	

source 1.38  
/organism="unknown"  
/mol\_type="unassigned RNA"  
ORIGIN

Query Match 77.4%; Score 29.4; DB 6; Length 38;  
Best Local Similarity 80.6%; Pred. No. 0.098;  
Matches 25; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AAUCUGAUGAGCGCGUAGCGCGAATAUCA 36  
Db 6 AAACGATGAGCGCGGTTAGCGCGAATAUCA 36

Search completed: May 13, 2005, 18:17:11  
Job time : 1091.95 secs

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XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
PT constructs, which down regulate expression of a CD20 gene or neurite  
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
PT central nervous system injury.

XX  
PS Claim 89; Page 74; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates  
CC expression of a CD20 gene and a nucleic acid molecule which down  
CC regulates expression of a neurite growth inhibitor gene (NOCO). The  
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
CC DNAzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule  
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
CC an amberzyme (cleaving RNA with an NGN triplet), a zynzyme (cleaving RNA  
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
CC of CD20 in the presence of a divalent cation that is preferably  $Mg^{2+}$ .  
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
CC the cell and treat a patient having a condition associated with the level  
CC of CD20. The treatment may further comprise the use of one or more  
CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-  
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
CC leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
CC immune thrombocytopenia, and inflammatory arthropathy. The NOCO-  
CC targeting nucleic acid is used to cleave RNA of the NOCO gene in the  
CC presence of a divalent cation that is preferably  $Mg^{2+}$ . Furthermore, the  
CC nucleic acid may be contacted with a cell to reduce NOCO activity of the  
CC cell and treat a patient having a condition associated with the level of  
CC NOCO. The treatment may further comprise the use of one or more  
CC therapies. In particular, the NOCO-targeting nucleic acid may be used to  
CC treat central nervous system (CNS) injury and cerebrovascular accident  
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
CC disease, muscular dystrophy, and/or other neurodegenerative disease  
CC states which respond to the modulation of NOCO expression. The present  
CC sequence is a substrate sequence for a nucleic acid of the invention  
CC based on the human NOCO sequence

XX  
SQ Sequence 38 BP; 11 A; 9 C; 11 G; 0 T; 7 U; 0 Other;

XX Query Match 82.6%; Score 31.4; DB 4; Length 38;  
XX Best Local Similarity 97.0%; Pred. No. 0.00063;  
XX Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAUCUCGAGGAGCGCGUAGGCCGAAAAAUAUCAG 37  
DB |||||  
5 CAUCUCGAGGAGCGCGUAGGCCGAAAAAUAUCAG 37

RESULT 5  
ABL47321  
ID ABL47321 standard; RNA; 38 BP.  
XX  
XX ABL47321;  
AC  
XX  
XX 27-JUN-2003 (first entry)  
DT  
XX  
XX  
DE Human GR1D hammerhead ribozyme oligonucleotide #49.  
XX  
XX Human; Grb2-related with Insert Domain; GR1D; T-cell; ribozyme;  
KW co-stimulatory adaptor protein; tissue rejection; graft rejection;  
KW leukemia; cytosolic; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200162911-A2.  
FN  
XX  
XX 30-AUG-2001.  
PD  
XX  
XX 23-FEB-2001; 2001WO-US005957.  
PF

XX  
PR 24-FEB-2000; 2000US-0184594P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA  
PA (GLAX ) GLAXO GROUP LTD.  
XX  
XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;  
PI  
XX  
XX MPI; 2001-550088/61.  
DR  
XX  
XX  
PT New nucleic acid(s) for regulating the Grb2-related with Insert Domain  
PT (GR1D) gene comprises using antisense and enzymatic nucleic acid  
PT molecules such as hammerhead ribozymes.

XX  
PS Claim 5; Page 60; 108pp; English.

XX The present invention relates to oligonucleotides that downregulate the  
CC expression of human Grb2-related with Insert Domain (GR1D) gene. GR1D is  
CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful  
CC for modulating the expression of GR1D, to treat conditions such as  
CC tissue/graft rejection and leukemia. The oligonucleotides can also be  
CC administered in conjunction with other therapies such as radiation,  
CC chemotherapy and cyclosporin treatment. The present oligonucleotide was  
CC used to illustrate the invention

XX  
SQ Sequence 38 BP; 14 A; 7 C; 11 G; 0 T; 6 U; 0 Other;

XX Query Match 82.6%; Score 31.4; DB 4; Length 38;  
XX Best Local Similarity 97.0%; Pred. No. 0.00063;  
XX Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCAUUCGAGGAGCGCGUAGGCCGAAAAUAUCA 36  
DB |||||  
4 GCAUUCGAGGAGCGCGUAGGCCGAAAAUAUCA 36

RESULT 6  
ABK57933  
ID ABK57933 standard; RNA; 38 BP.  
XX  
XX  
XX ABK57933;  
AC  
XX  
XX 02-JUL-2002 (first entry)  
DT  
XX  
XX Human CLCA1 gene enzymatic nucleic acid #2304.  
DE  
XX  
XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
KW acetylcysteine.

XX  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200211674-A2.  
FN  
XX  
XX 14-FEB-2002.  
PD  
XX  
XX 09-AUG-2001; 2001WO-US024970.  
PF  
XX  
XX 09-AUG-2000; 2000US-0224383P.  
PR  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (SYNT ) SYNTEX USA LLC.  
PA (THOM/) THOMPSON J.  
XX  
XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;  
PI Grube A;  
XX  
XX MPI, 2002-217145/27.  
DR  
XX  
XX Enzymatic polynucleotide that down regulates expression of chloride  
PT channel calcium activated gene, useful for treating Chronic obstructive

PT pulmonary disease (COPD), chronic bronchitis and asthma.  
XX  
PS Claim 5; Page 55; 152pp; English.  
XX  
CC The invention relates to enzymatic nucleic acid molecules that down  
CC regulate expression of chloride channel calcium activated 1 (ClCA1) genes  
CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
CC useful as pharmaceutical agents for treating conditions such as chronic  
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
CC that are related to or will respond to the levels of ClCA1 in a cell or  
CC tissue. The sequences are useful for reducing ClCA1 activity in a cell,  
CC hence, are useful for treatment of a patient having a condition  
CC associated with the level of ClCA1, where the invention further comprises  
CC the use of one or more therapies under conditions suitable for the  
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
CC nucleic acids of the invention are also used as diagnostic tools to  
CC examine genetic drift and mutations within diseased cells or to detect  
CC the presence of ClCA1 RNA in a cell. This sequence represents an  
CC enzymatic nucleic acid molecule of the invention  
CC  
XX  
SQ Sequence 38 BP; 11 A; 7 C; 10 G; 0 T; 10 U; 0 Other;  
Query Match 82.6%; Score 31.4; DB 6; Length 38;  
Best Local Similarity 97.0%; Pred. No. 0.00063;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 UGCAUUCUGAUGAGCCGCUUAGCCGGAANAUC 35  
Db 3 UGAAAUUCUGAUGAGCCGCUUAGCCGGAANAUC 35  
RESULT 7  
ACDS2864  
ID ACDS2864 standard; RNA; 38 BP.  
XX  
AC ACDS2864;  
XX  
XX 24-SEP-2003 (first entry)  
DE HBV inozyme sequence #586.  
XX  
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
XX RNA stability; RNA expression; RNA synthesis; antisense;  
XX enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
XX amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
XX HBV reverse transcriptase; Enhancer I region; viral replication;  
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
XX vincristine; antiinflammatory; ss.  
XX  
OS Hepatitis B virus.  
XX  
PN WO200281494-A1.  
XX  
PD 17-OCT-2002.  
XX  
XX 26-MAR-2002; 2002WO-US009187.  
XX  
XX 26-MAR-2001; 2001US-00817879.  
XX  
XX 08-JUN-2001; 2001US-00877478.  
XX  
XX 08-JUN-2001; 2001US-0296876P.  
XX  
XX 24-OCT-2001; 2001US-0335059P.  
XX  
XX 05-DEC-2001; 2001US-0337055P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX (BLAT/) BLATT L.  
XX (MACE/) MACEJAK D.  
XX (MCSW/) MCSWIGGEN J.  
XX (MORR/) MORRISSEY D.  
XX (PAVC/) PAVCO P.  
XX (LEEB/) LEE P.

PA (DRAE/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX  
XX Blate L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX WPI, 2003-229207/22.  
DR  
XX Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX  
XX Example 1; Page 161; 387pp; English.  
PS  
XX  
XX The present invention relates to nucleic acid molecules which modulate  
XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
XX Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
XX and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
XX inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
XX are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
XX transcriptase and/or HBV reverse transcriptase primer sequences, as well  
XX as oligonucleotides that specifically bind the Enhancer I region of HBV  
XX DNA. The nucleic acids may be used to modulate the expression of HBV  
XX genes and HBV viral replication. Also disclosed is a method for screening  
XX compounds and/or potential therapies directed against HBV, and compounds  
XX that modulate the expression and/or replication of HCV. The compounds and  
XX methods of the invention are useful for the treatment of degenerative and  
XX disease states related to HBV and HCV infection, replication and gene  
XX expression such as cirrhosis, liver failure, and hepatocellular  
XX carcinoma. The present sequence represents one of the HBV ribozyme,  
XX inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences disclosed in  
XX the present invention  
SQ Sequence 38 BP; 11 A; 9 C; 10 G; 0 T; 7 U; 1 Other;  
Query Match 82.6%; Score 31.4; DB 8; Length 38;  
Best Local Similarity 94.1%; Pred. No. 0.00063;  
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CCUGCAUUCUGAUGAGCCGCUUAGCCGGAANAUC 34  
Db 1 CCUGCAUUCUGAUGAGCCGCUUAGCCGGAANAUC 34  
RESULT 8  
ADMS4641  
ID ADMS4641 standard; RNA; 38 BP.  
XX  
XX ADMS4641;  
XX  
XX 03-JUN-2004 (first entry)  
DE  
XX Hammerhead ribozyme targeting human GRID #49.  
XX  
XX Human; ss; GRID; Grid2-related with insert domain; hammerhead ribozyme;  
XX NCH ribozyme; G-cleaver ribozyme; zinzyme; DNazyme; amberzyme; Inozyme;  
XX hairpin ribozyme; tissue rejection; graft rejection; leukemia.  
XX  
XX Homo sapiens.  
XX Synthetic.  
OS  
XX  
XX US2003134806-A1.  
XX  
XX 17-UTL-2003.  
XX  
XX 23-FEB-2001; 2001US-00792818.  
XX  
XX 10-FEB-2000; 2000US-0181594P.  
XX  
XX (JARV/) JARVIS T.  
XX (CARL/) CARLOWITZ I V.  
XX (MCSW/) MCSWIGGEN J.  
XX (HAMB/) HAMBLIN P A.

PA (BLI/) ELIIS J. H.  
XX  
PI Jarvis T, Carlowitz IV, Mcswigen J, Hamblin PA, Ellis JH;  
XX WPI; 2003-829646/77.  
DR  
XX  
XX  
PT New nucleic acid molecule that down-regulates expression of Gb2-related  
PT with insert domain (GRID) gene, useful for treating a condition  
PT associated with the level of GRID, e.g. tissue/graft rejection and  
PT leukemia.  
PS  
XX  
XX Claim 5; SEQ ID NO 954; 74bp; English.  
XX  
XX The invention relates to a nucleic acid molecule that down-regulates  
XX expression of Gb2-related with insert domain (GRID) gene, e.g. a  
XX hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyme, DNzyme,  
XX amberzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell  
XX including the novel nucleic acid molecule, reducing GRID activity in a  
XX cell by contacting the cell with the novel nucleic acid molecule,  
XX creating a patient having a condition associated with the level of GRID  
XX (e.g. tissue/graft rejection or leukemia) by contacting the cell with  
XX the novel nucleic acid molecule, cleaving RNA of a GRID gene by  
XX contacting the cell with the novel nucleic acid molecule, an expression  
XX vector comprising a nucleic acid sequence (encoding at least the novel  
XX nucleic acid molecule in a manner that allows its expression), a  
XX mammalian cell including the expression vector and an enzymatic nucleic  
XX acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid  
XX molecule is useful for treating a condition associated with the level of  
XX GRID, e.g. tissue/graft rejection and leukemia. The present sequence is  
XX a hammerhead ribozyme of the invention.  
SQ  
XX Sequence 38 BP; 14 A; 7 C; 11 G; 0 T; 6 U; 0 Other;  
Query Match 82.6%; Score 31.4; DB 11; Length 38;  
Best Local Similarity 97.0%; Pred. No. 0.00063;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 GCAUUCGAGUGAGCGCGUUGAGCGCGAANAUA 36  
DB 4 GCAGUCUGAGUGAGCGCGUUGAGCGCGAANAUA 36  
RESULT 9  
ADM61662  
ID ADM61662 standard; RNA; 38 BP.  
AC  
XX ADM61662;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Hepatitis B virus (HBV) enzymatic nucleic acid #1254.  
XX  
XX Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;  
KW hepatitis B virus infection; hepatitis; hepatocellular carcinoma;  
KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;  
KW vironcide; hepatotropic; antiinflammatory; cytosolic.  
XX  
XX Hepatitis B virus.  
OS  
XX  
XX US2004054156-A1.  
PN  
XX  
XX 18-MAR-2004.  
PD  
XX  
XX 15-JAN-2003; 2003US-00342902.  
PF  
XX  
XX 14-MAY-1992; 92US-00982712.  
PR 07-FEB-1994; 94US-00193627.  
PR 08-NOV-1999; 99US-00436430.  
PR 20-MAR-2000; 2000US-00531025.  
PR 09-AUG-2000; 2000US-00636385.  
PR 24-OCT-2000; 2000US-00696347.  
PR 08-JUN-2001; 2001US-00877478.  
PR  
XX

PA (DRAP/) DRAPER K.  
XX (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGEN J A.  
XX (MORR/) MORRISSEY D.  
PI Draper K, Blatt L, Mcswigen JA, Morrissey D;  
XX WPI; 2004-247781/23.  
DR  
XX  
XX  
PT Novel enzymatic nucleic acid molecule such as DNzymes and inozymes  
PT specifically cleaving RNA derived from hepatitis B virus and comprising  
PT one or more binding arms, useful for treating hepatitis and cirrhosis.  
PS  
XX  
XX Disclosure; SEQ ID NO 3796; 122bp; English.  
XX  
XX The invention relates to an enzymatic nucleic acid molecule that  
XX specifically cleaves RNA derived from hepatitis B virus (HBV) and  
XX comprising one or more binding arms, without requiring the presence of a  
XX 2'-OH group within the molecule for activity. The nucleic acids are  
XX useful for treating hepatitis B virus infection, hepatitis,  
XX hepatocellular carcinoma, cirrhosis and liver failure, either alone or in  
XX combination with other therapies such as lamivudine and interferon. The  
XX nucleic acids are useful as diagnostic tools to examine genetic drift and  
XX mutations within diseased cells, for detecting the presence of HBV RNA in  
XX a cell, for the study of RNA and for down-regulating gene expression of  
XX target genes in bacterial, fungal, viral, plant or mammalian cells. This  
XX sequence represents an enzymatic nucleic acid molecule which cleaves HBV  
XX RNA of the invention. Note: The sequence data for this patent is also  
XX available in electronic format from USPTO at  
XX [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
SQ  
XX Sequence 38 BP; 11 A; 9 C; 10 G; 0 T; 7 U; 1 Other;  
Query Match 82.6%; Score 31.4; DB 12; Length 38;  
Best Local Similarity 94.1%; Pred. No. 0.00063;  
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CCUGCAUUCGAGUGAGCGCGUUGAGCGCGAANAUA 34  
DB 1 CCUGCAUUCGAGUGAGCGCGUUGAGCGCGAANAUA 34  
RESULT 10  
ACN26747  
ID ACN26747 standard; RNA; 38 BP.  
AC  
XX ACN26747;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE WNV minus strand Hammerhead Ribozyme SEQ ID NO 26763.  
XX  
XX WNV, West Nile Virus; antiinflammatory; cytosolic; hepatotropic;  
KW vironcide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNzyme;  
KW Amberzyme; Zinzyme; ss.  
XX  
XX  
XX West Nile Virus.  
OS  
XX  
XX WO200268637-A2.  
PN  
XX  
XX 06-SEP-2002.  
PD  
XX  
XX 19-OCT-2001; 2001WO-US048350.  
PF  
XX  
XX 20-OCT-2000; 2000US-0242411P.  
PR  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGEN J A.  
XX  
XX Blatt L, Mcswigen JA;  
PI

XX WPI; 2002-706994/76.  
XX  
XX New nucleic acid molecule that modulates replication of West Nile Virus  
XX (WNV), useful for treating a condition related to WNV infection e.g.  
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
XX Claim 24; SEQ ID NO 26763; 495bp; English.  
XX  
XX The invention relates to nucleic acid molecules that modulate replication  
XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
XX treating a condition related to WNV infection e.g. pancreatitis,  
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
XX molecule is selected from the group of ribozymes consisting of  
XX Hammerhead, Inozyme, G-cleaver, DNazyme, Ambenzyme and Zinzyme. The  
XX nucleic acid molecules further comprise at least five ribose residues, at  
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
XX least three of the 5' terminal nucleotides and a 3' end modification of a  
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
XX in the specification. The present sequence is that of a nucleic acid  
XX molecule of the invention  
XX  
XX Sequence 38 BP; 9 A; 10 C; 12 G; 0 T; 7 U; 0 Other;  
XX  
XX Query Match 82.1%; Score 31.2; DB 6; Length 38;  
XX Best Local Similarity 91.7%; Pred. No. 0.00078;  
XX Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
XX  
XX 2 CUGCAUUCUGAUGAGCGCCGUAAGCCGAAAUUACAG 37  
XX |||||  
XX 2 CUGCAGUCUGAUGAGCGCCGUAAGCCGAAAUACAG 37  
XX  
XX  
XX RESULT 11  
XX ACN27300  
XX ID ACN27300 standard; RNA; 38 BP.  
XX  
XX ACN27300;  
XX  
XX 22-APR-2004 (first entry)  
XX  
XX WNV minus strand Hammerhead Ribozyme SEQ ID NO 27316.  
XX  
XX WNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
XX virocidic; neuroprotective; antibacterial; replication; pancreatitis;  
XX encephalitis; myocarditis; meningitis; infection; hepatitis;  
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
XX Ambenzyme; Zinzyme; ss.  
XX  
XX West Nile Virus.  
XX  
XX WO200268637-A2.  
XX  
XX 06-SEP-2002.  
XX  
XX 19-OCT-2001; 2001WO-US048350.  
XX  
XX 20-OCT-2000; 2000US-0242411P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX (BLAT/) BLATT L.  
XX (MCSM/) MCSMIGEN J A.  
XX  
XX Blatt L, Mcawiggen JA;  
XX  
XX WPI; 2002-706994/76.  
XX  
XX New nucleic acid molecule that modulates replication of West Nile Virus  
XX (WNV), useful for treating a condition related to WNV infection e.g.  
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 24; SEQ ID NO 27316; 495bp; English.  
XX  
XX The invention relates to nucleic acid molecules that modulate replication  
XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
XX treating a condition related to WNV infection e.g. pancreatitis,  
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
XX molecule is selected from the group of ribozymes consisting of  
XX Hammerhead, Inozyme, G-cleaver, DNazyme, Ambenzyme and Zinzyme. The  
XX nucleic acid molecules further comprise at least five ribose residues, at  
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
XX least three of the 5' terminal nucleotides and a 3' end modification of a  
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
XX in the specification. The present sequence is that of a nucleic acid  
XX molecule of the invention  
XX  
XX Sequence 38 BP; 11 A; 6 C; 13 G; 0 T; 8 U; 0 Other;  
XX  
XX Query Match 82.1%; Score 31.2; DB 6; Length 38;  
XX Best Local Similarity 91.7%; Pred. No. 0.00078;  
XX Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
XX  
XX 3 UGCAUUCUGAUGAGCGCCGUAAGCCGAAAUUACAG 38  
XX |||||  
XX 3 UGCAUUCUGAUGAGCGCCGUAAGCCGAAAUACAG 38  
XX  
XX  
XX RESULT 12  
XX ACN26250  
XX ID ACN26250 standard; RNA; 38 BP.  
XX  
XX ACN26250;  
XX  
XX 22-APR-2004 (first entry)  
XX  
XX WNV minus strand Hammerhead Ribozyme SEQ ID NO 26266.  
XX  
XX WNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
XX virocidic; neuroprotective; antibacterial; replication; pancreatitis;  
XX encephalitis; myocarditis; meningitis; infection; hepatitis;  
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
XX Ambenzyme; Zinzyme; ss.  
XX  
XX West Nile Virus.  
XX  
XX WO200268637-A2.  
XX  
XX 06-SEP-2002.  
XX  
XX 19-OCT-2001; 2001WO-US048350.  
XX  
XX 20-OCT-2000; 2000US-0242411P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX (BLAT/) BLATT L.  
XX (MCSM/) MCSMIGEN J A.  
XX  
XX Blatt L, Mcawiggen JA;  
XX  
XX WPI; 2002-706994/76.  
XX  
XX New nucleic acid molecule that modulates replication of West Nile Virus  
XX (WNV), useful for treating a condition related to WNV infection e.g.  
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
XX Claim 24; SEQ ID NO 26266; 495bp; English.  
XX  
XX The invention relates to nucleic acid molecules that modulate replication  
XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
XX treating a condition related to WNV infection e.g. pancreatitis,  
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention

CC  
XX  
SQ Sequence 38 BP; 13 A; 9 C; 10 G; 0 T; 6 U; 0 Other;

Query Match 81.1%; Score 30.8; DB 6; Length 38;  
Best Local Similarity 94.1%; Pred. No. 0.0012;  
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 CAUCUGAUGAGCGCCGUAAGCCGAAAAUUCAG 38  
DB 5 CAGUCUGAUGAGCGCCGUAAGCCGAAAAUUCAG 38

RESULT 13  
ACN26622  
ID ACN26622 standard; RNA; 38 BP.

XX ACN26622;  
XX  
XX 22-APR-2004 (first entry)

XX  
XX  
XX MNV minus strand Hammerhead Ribozyme SEQ ID NO 26638.

XX  
XX  
XX MNV, West Nile Virus; antiinflammatory; cytosstatic; hepatotropic;  
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;  
XX encephalitis; myocarditis; meningitis; infection; hepatitis;  
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
XX Amberzyme; Zinzyme; ss.

XX  
XX  
XX West Nile Virus.

XX  
XX  
XX WO200268637-A2.

XX  
XX  
XX 06-SEP-2002.

XX  
XX  
XX 19-OCT-2001; 2001WO-US048350.

XX  
XX  
XX 20-OCT-2000; 2000US-0242411P.

XX  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX (BLAT/) BLATT L.  
XX (MCSW/) MCSWIGEN J A.

XX  
XX  
XX Blatt L, Mcswigen JA;  
XX  
XX  
XX MPI, 2002-706994/76.

XX  
XX  
XX New nucleic acid molecule that modulates replication of West Nile Virus  
XX (MNV), useful for treating a condition related to MNV infection e.g.  
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX  
XX  
XX Claim 24; SEQ ID NO 26638; 495bp; English.

XX  
XX  
XX The invention relates to nucleic acid molecules that modulate replication  
XX of the West Nile Virus (MNV). The nucleic acid molecules are useful for  
XX treating a condition related to MNV infection e.g. pancreatitis,  
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
XX molecule is selected from the group of ribozymes consisting of  
XX Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
XX nucleic acid molecules further comprise at least five ribose residues, at  
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
XX least three of the 5' terminal nucleotides and a 3' end modification of a  
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
XX in the specification. The present sequence is that of a nucleic acid  
XX molecule of the invention

CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention

CC  
XX  
SQ Sequence 38 BP; 12 A; 7 C; 14 G; 0 T; 5 U; 0 Other;

Query Match 80.5%; Score 30.6; DB 6; Length 38;  
Best Local Similarity 89.2%; Pred. No. 0.0014;  
Matches 33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 CUGCAUCUGAUGAGCGCCGUAAGCCGAAAAUUCAG 38  
DB 2 CUGCAGACUGAUGAGCGCCGUAAGCCGAAAAUUCAG 38

RESULT 14  
ACN27117  
ID ACN27117 standard; RNA; 38 BP.

XX ACN27117;  
XX  
XX 22-APR-2004 (first entry)

XX  
XX  
XX MNV minus strand Hammerhead Ribozyme SEQ ID NO 27133.

XX  
XX  
XX MNV, West Nile Virus; antiinflammatory; cytosstatic; hepatotropic;  
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;  
XX encephalitis; myocarditis; meningitis; infection; hepatitis;  
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
XX Amberzyme; Zinzyme; ss.

XX  
XX  
XX West Nile Virus.

XX  
XX  
XX WO200268637-A2.

XX  
XX  
XX 06-SEP-2002.

XX  
XX  
XX 19-OCT-2001; 2001WO-US048350.

XX  
XX  
XX 20-OCT-2000; 2000US-0242411P.

XX  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX (BLAT/) BLATT L.  
XX (MCSW/) MCSWIGEN J A.

XX  
XX  
XX Blatt L, Mcswigen JA;  
XX  
XX  
XX MPI, 2002-706994/76.

XX  
XX  
XX New nucleic acid molecule that modulates replication of West Nile Virus  
XX (MNV), useful for treating a condition related to MNV infection e.g.  
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX  
XX  
XX Claim 24; SEQ ID NO 27133; 495bp; English.

XX  
XX  
XX The invention relates to nucleic acid molecules that modulate replication  
XX of the West Nile Virus (MNV). The nucleic acid molecules are useful for  
XX treating a condition related to MNV infection e.g. pancreatitis,  
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
XX molecule is selected from the group of ribozymes consisting of  
XX Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
XX nucleic acid molecules further comprise at least five ribose residues, at  
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
XX least three of the 5' terminal nucleotides and a 3' end modification of a  
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
XX in the specification. The present sequence is that of a nucleic acid  
XX molecule of the invention

XX  
XX  
SQ Sequence 38 BP; 13 A; 7 C; 13 G; 0 T; 5 U; 0 Other;

Query Match 80.5%; Score 30.6; DB 6; Length 38;  
Best Local Similarity 89.2%; Pred. No. 0.0014;

	Matches	33, Conservative	0, Mismatches	4, Indels	0, Gaps
QY	2	CUCGAUCUGAUGAGCCGUGAGCCGAAAAUACAG	38		
Db	2	CUCGAAACUGAUGAGCCGUGAGCCGAAAAAGAAAG	38		

Matches	33;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

```

QY      1  CCUGCAUUCGUAUGAGGCCGUAAGCCGCAAAAAUACG  37
      - - - - - | | | | | | | | | | | | | | | | | |
Db      1  CUUGCGAUCUGAUGAGGCCGUAAGCCGCAAAAAUACUG  37

```

CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably  $Mg^{2+}$ . Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke). Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is a substrate sequence for a nucleic acid of the invention  
 CC based on the human CD20 sequence

XX Sequence 38 BP; 10 A; 8 C; 10 G; 0 T; 10 U; 0 Other;

Query Match 80.0%; Score 30.4; DB 4; Length 38;

Best Local Similarity 96.9%; Pred. No. 0.0018; Mismatches 1; Indels 0; Gaps 0;

Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

5 CAUUCGAGAGGCGCGUAGGCCGAAAUAUCA 36

5 CAUUCGAGAGGCGCGUAGGCCGAAAUAUCA 36

RESULT 17  
 ID ABRK05084 standard; RNA; 38 BP.

XX ABRK05084;

DT 12-MAR-2002 (first entry)

Human NOGO Inozyme substrate sequence #561.

Human; ss; antisense therapy; cytosolic; antiinflammatory; haemostatic;  
 CC cerebroprotective; neurotrophic; neuroprotective; antiparkinsonian;  
 CC muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 CC DNazyme; inozyme; G-cleaver; amberyze; zinzyme; lymphoma; leukaemia;  
 CC B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 CC human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 CC MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
 CC inflammatory arthropathy; central nervous system injury;  
 CC cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 CC chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 CC Parkinson's disease; ataxia; Huntington's disease; substrate sequence;  
 CC Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.

OS Synthetic.

XX WO200159103-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

XX 28-FEB-2000; 2000US-018516P.

XX 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT) BLATT L.

XX (MCSW) MCSWIGGEN J.

XX (CHOW) CHOWIRRA B M.

XX Blatt L, Mcawiggen J, Chowirra BM;

DR WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 CC constructs, which down regulate expression of a CD20 gene or neurite  
 CC growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 CC central nervous system injury.

XX Claim 89; Page 86; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NNN motif) or  
 CC an amberyze (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably  $Mg^{2+}$ .  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably  $Mg^{2+}$ . Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke). Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is a substrate sequence for a nucleic acid of the invention  
 CC based on the human NOGO sequence

XX Sequence 38 BP; 10 A; 8 C; 9 G; 0 T; 10 U; 1 Other;

Query Match 80.0%; Score 30.4; DB 4; Length 38;

Best Local Similarity 93.9%; Pred. No. 0.0018; Mismatches 2; Indels 0; Gaps 0;

Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 CUGCAUUCGAGAGGCGCGUAGGCCGAAAUAU 34

2 CUGCAUUCGAGAGGCGCGUAGGCCGAAAUAU 34

RESULT 18

ID ABRK04387 standard; RNA; 38 BP.

XX ABRK04387;

DT 12-MAR-2002 (first entry)

Human NOGO Hammerhead ribozyme substrate sequence #594.

Human; ss; antisense therapy; cytosolic; antiinflammatory; haemostatic;  
 CC cerebroprotective; neurotrophic; neuroprotective; antiparkinsonian;  
 CC muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 CC DNazyme; inozyme; G-cleaver; amberyze; zinzyme; lymphoma; leukaemia;  
 CC B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 CC human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 CC MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
 CC inflammatory arthropathy; central nervous system injury;  
 CC cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 CC chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;

KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;  
KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
OS Homo sapiens.  
XX Synthetic.  
XX WO200159103-A2.  
XX  
XX 16-AUG-2001.  
XX  
XX 09-FEB-2001; 2001WO-US004273.  
XX  
XX 11-FEB-2000; 2000US-0181797P.  
PR 28-FEB-2000; 2000US-0185516P.  
PR 06-MAR-2000; 2000US-0187128P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLATT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J.  
PA (CHOW/) CHOWRIRA B M.  
XX  
PI Blatt L, Mcswiggen J, Chowrira BM;  
XX  
XX WPI; 2001-607195/69.  
XX  
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
PT constructs, which down regulate expression of a CD20 gene or neurite  
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
PT central nervous system injury.  
XX  
XX Claim 89; Page 75; 200P; English.  
XX  
XX The invention relates to a nucleic acid molecule which down regulates  
CC expression of a CD20 gene and a nucleic acid molecule which down  
CC regulates expression of a neurite growth inhibitor gene (NOCO). The  
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
CC DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule  
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
CC an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA  
CC with a XGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
CC the cell and treat a patient having a condition associated with the level  
CC of CD20. The treatment may further comprise the use of one or more  
CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-  
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
CC immune thrombocytopenia, and inflammatory arthropathy. The NOCO-  
CC targeting nucleic acid is used to cleave RNA of the NOCO gene in the  
CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
CC nucleic acid may be contacted with a cell to reduce NOCO activity of the  
CC cell and treat a patient having a condition associated with the level of  
CC NOCO. The treatment may further comprise the use of one or more  
CC therapies. In particular, the NOCO-targeting nucleic acid may be used to  
CC treat central nervous system (CNS) injury and cerebrovascular accident  
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
CC disease, muscular dystrophy, and/or other neurodegenerative disease  
CC states which respond to the modulation of NOCO expression. The present  
CC sequence is a substrate sequence for a nucleic acid of the invention  
CC based on the human NOCO sequence  
XX  
XX Sequence 38 BP; 13 A; 9 C; 9 G; 0 T; 7 U; 0 Other;

Query Match 80.0%; Score 30.4; DB 4; Length 38;  
Best Local Similarity 96.9%; Pred. No. 0.0018;  
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAACUCGAGAGCCGCUUAGCCGCAAAAUAUCA 36  
|||||  
|||||

DB 5 CAACUCGAGAGCCGCUUAGCCGCAAAAUAUCA 36  
RESULT 19  
ACN29362  
ID ACN29362 standard; RNA, 38 BP.  
XX  
XX ACN29362;  
XX  
XX 22-APR-2004 (first entry)  
XX  
XX WNV minus strand Inozyme SEQ ID NO 29378.  
XX  
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KM encephalitis; myocarditis; meningitis; infection; hepatitis;  
KM liver failure; cancer; cirrhosis; Hammanhead; Inozyme; DNAzyme;  
KM Amberzyme; Zinczyme; ss.  
XX  
XX West Nile Virus.  
XX  
XX WO200268637-A2.  
XX  
XX 06-SEP-2002.  
XX  
XX 19-OCT-2001; 2001WO-US048350.  
XX  
XX 20-OCT-2000; 2000US-0242411P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLATT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J A.  
XX  
XX Blatt L, Mcswiggen JA;  
XX  
XX WPI; 2002-706394/76.  
XX  
XX New nucleic acid molecule that modulates replication of West Nile Virus  
PT (WNV), useful for treating a condition related to WNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
XX Claim 24; SEQ ID NO 29378; 495P; English.  
XX  
XX The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
CC treating a condition related to WNV infection e.g. pancreatitis, hep-  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammanhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and zinczyme. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention  
XX  
XX Sequence 38 BP; 11 A; 7 C; 11 G; 0 T; 8 U; 1 Other;

Query Match 80.0%; Score 30.4; DB 6; Length 38;  
Best Local Similarity 93.9%; Pred. No. 0.0018;  
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCAUCUGAGAGCCGCUUAGCCGCAAAAUAUCA 36  
|||||  
|||||

DB 4 GCAUCUGAGAGCCGCUUAGCCGCAAAAUAUCA 36  
|||||  
|||||

RESULT 20  
ABK04516  
ID ABK04516 standard; RNA; 38 BP.  
XX

AC ABR04516;  
XX  
XX 12-MAR-2002 (first entry)  
XX  
DE Human NOGO Hammerhead ribozyme substrate sequence #723.  
XX  
KM Human; 89; antisense therapy; cyostatic; antiinflammatory; haemostatic;  
KM cerebroprotective; neurotrophic; neuroprotective; antiparkinsonian;  
KM muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
KM DNAzyme; Inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;  
KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
KM MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
KM inflammatory arthropathy; central nervous system injury;  
KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
KM chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
KM Parkinson's disease; ataxia; Huntington's disease; substrate sequence;  
KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX WO200159103-A2.  
XX  
XX 16-AUG-2001.  
XX  
XX 09-FEB-2001; 2001WO-US004273.  
XX  
XX 11-FEB-2000; 2000US-0181797P.  
XX 28-FEB-2000; 2000US-0185516P.  
XX 06-MAR-2000; 2000US-0187128P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX (BLAT/) BLATT L.  
XX (MCSM/) MCSWIGEN J.  
XX (CHOW/) CHOWRIRA B M.  
XX  
XX Blatt L, Mcswigen J, Chowira BM;  
XX WPI; 2001-607195/69.  
XX  
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
XX constructs, which down regulate expression of a CD20 gene or neurite  
XX growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
XX central nervous system injury.  
XX  
XX Claim 89; Page 77; 200pp; English.  
XX  
XX The invention relates to a nucleic acid molecule which down regulates  
XX expression of a CD20 gene and a nucleic acid molecule which down  
XX regulates expression of a neurite growth inhibitor gene (NOGO). The  
XX nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
XX DNAzyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule  
XX possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
XX an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
XX with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
XX of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
XX Furthermore, it may be contacted with a cell to reduce CD20 activity of  
XX the cell and treat a patient having a condition associated with the level  
XX of CD20. The treatment may further comprise the use of one or more  
XX therapies. In particular, the CD20 targeting nucleic acid may be used to  
XX treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
XX Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
XX leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
XX lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
XX immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
XX targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
XX presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
XX nucleic acid may be contacted with a cell to reduce NOGO activity of the  
XX cell and treat a patient having a condition associated with the level of  
XX NOGO. The treatment may further comprise the use of one or more  
XX therapies. In particular, the NOGO-targeting nucleic acid may be used to  
XX treat central nervous system (CNS) injury and cerebrovascular accident

CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
CC disease, muscular dystrophy, and/or other neurodegenerative disease  
CC states which respond to the modulation of NOGO expression. The present  
CC sequence is a substrate sequence for a nucleic acid of the invention  
CC based on the human NOGO sequence  
XX  
SQ Sequence 38 BP; 13 A; 8 C; 10 G; 0 T; 7 U; 0 Other;  
XX  
Query Match 79.5%; Score 30.2; DB 4; Length 38;  
Best Local Similarity 91.4%; Pred. No. 0.0022;  
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
QY 2 CUGCAUCGAGUGAGCCGUGUAGCCGAAAUAUCA 36  
DB 2 CUGCAACUGAGUGAGCCGUGUAGCCGAAAUAUCA 36  
XX  
RESULT 21  
ACN26549  
ID ACN26549 standard; RNA; 38 BP.  
XX  
XX ACN26549;  
XX  
XX 22-APR-2004 (first entry)  
XX  
XX MNV minus strand Hammerhead Ribozyme SEQ ID NO 26565.  
XX  
XX MNV, West Nile Virus; antiinflammatory; cyostatic; hepatotropic;  
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;  
XX encephalitis; myocarditis; meningitis; infection; hepatitis;  
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
XX Amberzyme; zinzyme; ss.  
XX  
XX West Nile Virus.  
XX  
XX WO200268637-A2.  
XX  
XX 06-SEP-2002.  
XX  
XX 19-OCT-2001; 2001WO-US048350.  
XX  
XX 20-OCT-2000; 2000US-0242411P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX (BLAT/) BLATT L.  
XX (MCSM/) MCSWIGEN J A.  
XX  
XX Blatt L, Mcswigen JA;  
XX WPI; 2002-706994/76.  
XX  
XX New nucleic acid molecule that modulates replication of West Nile Virus  
XX (MNV), useful for treating a condition related to MNV infection e.g.  
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
XX Claim 24; SEQ ID NO 26565; 495pp; English.  
XX  
XX The invention relates to nucleic acid molecules that modulate replication  
XX of the West Nile Virus (MNV). The nucleic acid molecules are useful for  
XX treating a condition related to MNV infection e.g. pancreatitis,  
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
XX molecule is selected from the group of ribozymes consisting of  
XX Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and zinzyme. The  
XX nucleic acid molecules further comprise at least five ribose residues, at  
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
XX least three of the 5' terminal nucleotides and a 3' end modification of a  
XX 3',3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
XX in the specification. The present sequence is that of a nucleic acid  
XX molecule of the invention

XX Sequence 38 BP; 11 A; 6 C; 14 G; 0 T; 7 U; 0 Other;  
SQ  
Query Match 79.5%; Score 30.2; DB 6; Length 38;  
Best Local Similarity 91.4%; Pred. No. 0.0022; 3; Indels 0; Gaps 0;  
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 4 GCATUCGAGGCGGUAAGCGGAAAUACAG 38  
DB 4 GCATUCGAGGCGGUAAGCGGAAAUACAG 38  
RESULT 22  
ACN30394  
ID ACN30394 standard; RNA; 38 BP.  
XX ACN30394;  
AC ACN30394;  
XX 22-APR-2004 (first entry)  
DT  
XX WNV minus strand Inozyme SEQ ID NO 30410.  
DE  
XX WNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KM encephalitis; myocarditis; meningitis; infection; hepatitis;  
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
KM Amberzyme; Zinzyme; ss.  
XX  
OS West Nile Virus.  
XX  
PN WO200268637-A2.  
XX  
PD 06-SEP-2002.  
XX  
XX 19-OCT-2001; 2001WO-US048350.  
XX  
XX 20-OCT-2000; 2000US-0242411P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX (BLAT/) BLATT L.  
XX (MCSW/) MCSWIGEN J A.  
XX  
XX Blatt L, Mcswigen JA;  
PI  
DR WPI; 2002-706994/76.  
XX  
XX New nucleic acid molecule that modulates replication of West Nile Virus  
PT (WNV), useful for treating a condition related to WNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
XX Claim 24; SEQ ID NO 30410; 495pp; English.  
XX  
XX The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
CC treating a condition related to WNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention  
XX  
SQ Sequence 38 BP; 9 A; 9 C; 11 G; 0 T; 8 U; 1 Other;  
XX  
Query Match 79.5%; Score 30.2; DB 6; Length 38;  
Best Local Similarity 88.9%; Pred. No. 0.0022; 4; Indels 0; Gaps 0;  
Matches 32; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CUGCAUUCGAGGCGGUAAGCGGAAAUACAG 37  
DB 2 CUGCCUUCGAGGCGGUAAGCGGAAAUACAG 37  
RESULT 23  
AAH96054  
ID AAH96054 standard; RNA; 38 BP.  
XX AAH96054;  
AC AAH96054;  
XX 09-OCT-2001 (first entry)  
DT  
XX Human Chk1 ribozyme SEQ ID NO: 1479.  
DE  
XX Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;  
KM RNA cleavage; cancer; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200157206-A2.  
XX  
XX 09-AUG-2001.  
PD  
XX 02-FEB-2001; 2001WO-US003504.  
XX  
XX 03-FEB-2000; 2000US-0179983P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX (PART/) FATTAEY A R.  
XX  
XX Fattaey AR, Jarvis T, Mcswigen J, Booher RN, Holman PS;  
XX  
XX WPI; 2001-496922/54.  
XX  
XX Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid  
PT molecules, which downregulates expression of a checkpoint kinase-1 gene,  
PT useful for treating colorectal, lung, breast or prostate cancers.  
XX  
XX Claim 5; Page 53; 115pp; English.  
XX  
XX The present invention provides nucleic acid molecules capable of  
CC downregulating the expression of the human checkpoint kinase-1 (Chk1)  
CC gene. These may be antisense or ribozyme sequences, and are useful in the  
CC treatment of diseases associated with conditions affected by Chk1 levels,  
CC including cancer. The present sequence is an oligonucleotide described in  
CC the exemplification of the invention  
XX  
SQ Sequence 38 BP; 8 A; 9 C; 12 G; 0 T; 9 U; 0 Other;  
XX  
Query Match 78.9%; Score 30; DB 4; Length 38;  
Best Local Similarity 86.8%; Pred. No. 0.0026; 5; Indels 0; Gaps 0;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 CCUGCAUUCGAGGCGGUAAGCGGAAAUACAG 38  
DB 1 CCUGCAUUCGAGGCGGUAAGCGGAAAUACAG 38  
RESULT 24  
ABK58289  
ID ABK58289 standard; RNA; 38 BP.  
XX  
XX ABK58289;  
AC  
XX 02-JUL-2002 (first entry)  
DT  
XX Human CLKAI gene enzymatic nucleic acid #2660.  
XX  
XX Human; chloride channel activated 1; CLKAI; ss; antiasthmatic;  
KM antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
KM chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
KM oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;

KM acetylcysteine.  
XX  
OS Homo sapiens.  
XX  
PN WO200211674-A2.  
XX  
PD 14-FEB-2002.  
XX  
PF 09-AUG-2001; 2001WO-US024970.  
XX  
PR 09-AUG-2000; 2000US-0224383P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (SYNT) SYNTX USA LLC.  
PA (THOM/) THOMPSON J.  
PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;  
PI Grube A;  
XX WPI; 2002-217145/27.  
XX  
XX Enzymatic polynucleotide that down regulates expression of chloride  
PT channel calcium activated gene, useful for treating Chronic obstructive  
PT pulmonary disease (COPD), chronic bronchitis and asthma.  
XX  
XX Claim 5; Page 61; 152pp; English.  
XX  
XX The invention relates to enzymatic nucleic acid molecules that down  
CC regulate expression of chloride channel calcium activated 1 (ClCA1) genes  
CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
CC useful as pharmaceutical agents for treating conditions such as chronic  
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
CC that are related to or will respond to the levels of ClCA1 in a cell or  
CC tissue. The sequences are useful for reducing ClCA1 activity in a cell,  
CC hence, are useful for treatment of a patient having a condition  
CC associated with the level of ClCA1, where the invention further comprises  
CC the use of one or more therapies under conditions suitable for the  
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
CC nucleic acids of the invention are also used as diagnostic tools to  
CC examine genetic drift and mutations within diseased cells or to detect  
CC the presence of ClCA1 RNA in a cell. This sequence represents an  
CC enzymatic nucleic acid molecule of the invention  
XX  
SQ Sequence 38 BP; 14 A; 7 C; 10 G; 0 T; 7 U; 0 Other;  
XX  
Query Match 78.9%; Score 30; DB 6; Length 38;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 4 GCAUUCUGAUGAGCCGUTUAGCCGAAAAA 33  
DB 4 GCAUUCUGAUGAGCCGUTUAGCCGAAAAA 33  
XX  
RESULT 25  
ID ACN26440 standard; RNA; 38 BP.  
XX  
AC ACN26440;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE WNV minus strand Hammerhead Ribozyme SEQ ID NO 26456.  
XX  
XX WNV; West Nile Virus; antiinflammatory; cyrostatic; hepatotropic;  
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KM encephalitis; myocarditis; meningitis; infection; hepatitis;  
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
KM Amberzyme; Zinzyne; ss.  
XX  
OS West Nile Virus.  
XX

XX  
PN WO200268637-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 19-OCT-2001; 2001WO-US048350.  
XX  
PR 20-OCT-2000; 2000US-0242411P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J A.  
PI Blatt L, Mcswiggen JA;  
XX WPI; 2002-706994/76.  
XX  
XX New nucleic acid molecule that modulates replication of West Nile Virus  
PT (WNV), useful for treating a condition related to WNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
XX Claim 24; SEQ ID NO 26456; 495pp; English.  
XX  
XX The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
CC treating a condition related to WNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3',3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention  
XX  
SQ Sequence 38 BP; 12 A; 8 C; 13 G; 0 T; 5 U; 0 Other;  
XX  
Query Match 78.9%; Score 30; DB 6; Length 38;  
Best Local Similarity 86.8%; Pred. No. 0.0026;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
XX  
QY 1 CCUGCAUUCUGAUGAGCCGUTUAGCCGAAAAAUCAGG 38  
DB 1 CCAGGACUCUGAUGAGCCGUTUAGCCGAAAAAAGAG 38  
XX  
RESULT 26  
ID ACN26144 standard; RNA; 38 BP.  
XX  
AC ACN26144;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE WNV minus strand Hammerhead Ribozyme SEQ ID NO 26160.  
XX  
XX WNV; West Nile Virus; antiinflammatory; cyrostatic; hepatotropic;  
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KM encephalitis; myocarditis; meningitis; infection; hepatitis;  
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
KM Amberzyme; Zinzyne; ss.  
XX  
OS West Nile Virus.  
XX  
XX WO200268637-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 19-OCT-2001; 2001WO-US048350.  
XX



XX OS Homo sapiens.  
XX PN WO200281628-A2.  
XX PD 17-OCT-2002.  
XX PF 03-APR-2002; 2002WO-US010512.  
XX PR 05-APR-2001; 2001US-00827395.  
XX PR 29-MAY-2001; 2001US-0294412P.  
XX PR 28-AUG-2001; 2001US-0315315P.  
XX PA (RIBO-) RIBOZYME PHARM INC.  
XX PI Blatt L, Chowrira B, Haeblerl P, Mcswiggen J, Fosnaugh K;  
XX DR WPI; 2003-058513/05.  
XX PT Novel enzymatic nucleic acid that down-regulates expression of neurite  
XX growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or  
XX protein kinase PKR genes, for treating cancer and inflammatory disease.  
XX PS Claim 57; SEQ ID NO 7084; 317pp; English.  
XX CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)  
XX that down regulate the expression or inhibit the function of a receptor  
XX for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),  
XX Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the  
XX invention are useful for treating: cerebrovascular accident, central  
XX nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,  
XX lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,  
XX restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune  
XX disease, lupus, multiple sclerosis, transplant/graft rejection,  
XX ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic  
XX conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The  
XX nucleic acids of the invention are also useful for down-regulating the  
XX expression of a target gene and as a diagnostic tool to examine genetic  
XX drifts and mutations within diseased cells or to detect the presence of a  
XX target RNA in a cell. The present RNA sequence represents a human IKK-  
XX gamma ribozyme sequence.  
SQ Sequence 38 BP; 8 A; 9 C; 13 G; 0 T; 8 U; 0 Other;  
Query Match 78.9%; Score 30; DB 11; Length 38;  
Best Local Similarity 86.8%; Pred. No. 0.0026;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 CCUGCAUUCUGAUGAGCGCGUUGAGCCGAAAUAUACAG 38  
Db 1 CCUGUUCUGAUGAGCGCGUUGAGCCGAAAUAUACAG 38  
RESULT 29  
ADL55719  
ID ADL55719 standard; RNA; 38 BP.  
AC ADL55719;  
XX  
XX  
DT 20-MAY-2004 (first entry)  
XX  
XX Human PKR ribozyme sequence #183.  
DE  
XX antisense oligonucleotide; neurite growth inhibitor; NOGO;  
KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;  
KW protein kinase PKR; cerebrovascular accident;  
KW central nervous system injury; CNS injury; spinal cord injury; cancer;  
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;  
KW restenosis; asthma; Crohn's disease; diabetes; obesity;  
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;  
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;  
KW allergy; asthma; allergic rhinitis; atopic dermatitis; PKR ribozyme;  
KW substrate; ss; human.

XX OS Homo sapiens.  
XX PN WO200281628-A2.  
XX PD 17-OCT-2002.  
XX PF 03-APR-2002; 2002WO-US010512.  
XX PR 05-APR-2001; 2001US-00827395.  
XX PR 29-MAY-2001; 2001US-0294412P.  
XX PR 28-AUG-2001; 2001US-0315315P.  
XX PA (RIBO-) RIBOZYME PHARM INC.  
XX PI Blatt L, Chowrira B, Haeblerl P, Mcswiggen J, Fosnaugh K;  
XX DR WPI; 2003-058513/05.  
XX PT Novel enzymatic nucleic acid that down-regulates expression of neurite  
XX growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or  
XX protein kinase PKR genes, for treating cancer and inflammatory disease.  
XX PS Claim 57; SEQ ID NO 9252; 317pp; English.  
XX CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)  
XX that down regulate the expression or inhibit the function of a receptor  
XX for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),  
XX Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the  
XX invention are useful for treating: cerebrovascular accident, central  
XX nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,  
XX lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,  
XX restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune  
XX disease, lupus, multiple sclerosis, transplant/graft rejection,  
XX ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic  
XX conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The  
XX nucleic acids of the invention are also useful for down-regulating the  
XX expression of a target gene and as a diagnostic tool to examine genetic  
XX drifts and mutations within diseased cells or to detect the presence of a  
XX target RNA in a cell. The present RNA sequence represents a human PKR  
XX ribozyme sequence.  
SQ Sequence 38 BP; 11 A; 7 C; 8 G; 0 T; 12 U; 0 Other;  
Query Match 78.9%; Score 30; DB 11; Length 38;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 AAUCUGAUGAGCGCGUUGAGCCGAAAUAUAC 35  
Db 6 AAUCUGAUGAGCGCGUUGAGCCGAAAUAUAC 35  
RESULT 30  
ADM60497  
ID ADM60497 standard; RNA; 38 BP.  
AC ADM60497;  
XX  
XX  
DT 03-JUN-2004 (first entry)  
XX  
XX Hepatitis B virus (HBV) enzymatic nucleic acid #89.  
DE  
XX Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;  
KW Hepatitis B virus infection; hepatitis; hepatocellular carcinoma;  
KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;  
KW virus; hepatotropic; antiinflammatory; cytostatic.  
XX  
XX Hepatitis B virus.  
XX OS  
XX US2004054156-A1.  
XX PN  
XX 18-MAR-2004.

XX 15-JAN-2003; 2003US-00342902.  
XX  
XX 14-MAY-1992; 92US-00882712.  
PR 07-FEB-1994; 94US-00193627.  
PR 08-NOV-1999; 99US-00436430.  
PR 20-MAR-2000; 2000US-00531025.  
PR 09-AUG-2000; 2000US-00636385.  
PR 24-OCT-2000; 2000US-00696347.  
PR 08-JUN-2001; 2001US-00877478.  
XX  
XX (DRAP/) DRAPER K.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGEN J. A.  
PA (MORR/) MORRISSEY D.  
XX  
XX Draper K, Blatt L, Mcswigen JA, Morrissey D;  
XX WPI; 2004-247781/23.  
XX  
XX Novel enzymatic nucleic acid molecule such as DNAses and inozymes  
PT specifically cleaving RNA derived from hepatitis B virus and comprising  
PT one or more binding arms, useful for treating hepatitis and cirrhosis.  
XX  
XX Disclosure; SEQ ID NO 2631; 122pp; English.  
XX  
XX The invention relates to an enzymatic nucleic acid molecule that  
CC specifically cleaves RNA derived from hepatitis B virus (HBV) and  
CC comprising one or more binding arms, without requiring the presence of a  
CC 2'-OH group within the molecule for activity. The nucleic acids are  
CC useful for treating hepatitis B virus infection, hepatitis,  
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in  
CC combination with other therapies such as lamivudine and interferons. The  
CC nucleic acids are useful as diagnostic tools to examine genetic drift and  
CC mutations within diseased cells, for detecting the presence of HBV RNA in  
CC a cell, for the study of RNA and for down-regulating gene expression of  
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This  
CC sequence represents an enzymatic nucleic acid molecule which cleaves HBV  
CC RNA of the invention. Note: The sequence data for this patent is also  
CC available in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html.  
XX  
XX  
XX Sequence 38 BP; 12 A; 8 C; 13 G; 0 T; 5 U; 0 Other;  
SQ  
Query Match 78.9%; Score 30; DB 12; Length 38;  
Best Local Similarity 86.8%; Pred. No. 0.0026; Mismatches 5; Indels 0; Gaps 0;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 CCUGCAUUCUGAUGAGCCGCUUAGCCGGAAGAAUACAG 38  
DB 1 CCAACAAGCUGAUGAGCCGCUUAGCCGGAAGAAUACAG 38  
RESULT 31  
ABK07861  
ID ABK07861 standard; RNA; 38 BP.  
XX  
XX ABK07861;  
AC  
XX  
XX 12-MAR-2002 (first entry)  
DT  
XX  
XX Human CD20 Hammerhead ribozyme substrate sequence #104.  
DE  
XX  
XX Human; 88; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
KW cerebroprotective; neurotrophic; neuroprotective; antiparkinsonian;  
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
KW DNAsyme; inozyme; G-cleaver; amberyzyme; zinzyme; lymphoma; leukaemia;  
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
KW MCL; immunodeficiency; IMC; immune thrombocytopenia; stroke; dementia;  
KW inflammatory arthropathy; central nervous system injury;  
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;

KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;  
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
XX  
XX OS Homo sapiens.  
OS Synthetic.  
XX  
XX WO200159103-A2.  
XX  
XX 16-AUG-2001.  
XX  
XX  
XX 09-FEB-2001; 2001WO-US004273.  
PF  
XX  
XX 11-FEB-2000; 2000US-0181797P.  
PR 28-FEB-2000; 2000US-0185516P.  
PR 06-MAR-2000; 2000US-0187128P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGEN J. A.  
PA (CHOW/) CHOWRITA B M.  
XX  
XX Blatt L, Mcswigen J, Chowrita BM;  
XX WPI; 2001-607195/69.  
XX  
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
PT constructs, which down regulate expression of a CD20 gene or neurite  
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
PT central nervous system injury.  
XX  
XX Claim 31; Page 141; 200pp; English.  
XX  
XX The invention relates to a nucleic acid molecule which down regulates  
CC expression of a CD20 gene and a nucleic acid molecule which down  
CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
CC DNAsyme) an inozyme (an endolytic nucleic acid cleaving an NNN motif) or  
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NNN motif) or  
CC an amberyzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
CC with a XGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
CC the cell and treat a patient having a condition associated with the level  
CC of CD20. The treatment may further comprise the use of one or more  
CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-  
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
CC cell and treat a patient having a condition associated with the level of  
CC NOGO. The treatment may further comprise the use of one or more  
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
CC treat central nervous system (CNS) injury and cerebrovascular accident  
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
CC disease, muscular dystrophy, and/or other neurodegenerative disease  
CC states which respond to the modulation of NOGO expression. The present  
CC sequence is a substrate sequence for a nucleic acid of the invention  
CC based on the human CD20 sequence  
XX  
XX Sequence 38 BP; 11 A; 8 C; 10 G; 0 T; 9 U; 0 Other;  
SQ  
Query Match 78.4%; Score 29.8; DB 4; Length 38;  
Best Local Similarity 93.9%; Pred. No. 0.0032; Mismatches 2; Indels 0; Gaps 0;  
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CUGCAUUCUGAUGAGCCGCUUAGCCGGAAGAAU 34  
|| |||||

DB 2 CUCUAUUGAGGCGGUAGGCCGAAAAAU 34

RESULT 32  
ABK04290  
ID ABK04290 standard; RNA; 38 BP.  
XX  
AC ABK04290;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Human NCOG Hammerhead ribozyme substrate sequence #497.  
XX  
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
XX cerebrioprotective; neurotropic; neuroprotective; antiparkinsonian;  
XX muscular; CD20; neurite growth inhibitor gene; NCOG; hammerhead ribozyme;  
XX DNazyme; inozyme; G-cleaver; amberyne; zinzyme; lymphoma; leukaemia;  
XX B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
XX human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
XX MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
XX inflammatory arthropathy; central nervous system injury;  
XX cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
XX chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
XX Parkinson's disease; ataxia; Huntington's disease; substrate sequence;  
XX Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
XX  
XX Homo sapiens.  
XX Synthetic.  
XX WO200159103-A2.  
XX  
XX 16-AUG-2001.  
XX  
XX 09-FEB-2001; 2001WO-US004273.  
XX  
XX 11-FEB-2000; 2000US-0181797P.  
XX 28-FEB-2000; 2000US-0185516P.  
XX 06-MAR-2000; 2000US-0187128P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX (BLAT/) BLATT L.  
XX (MCSW/) MCSWIGGEN J.  
XX (CHOW/) CHOWRIRA B M.  
XX  
XX Blatt L, Mcswiggen J, Chowrira BM;  
XX WPI; 2001-607195/69.  
XX  
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
XX constructs, which down regulate expression of a CD20 gene or neurite  
XX growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
XX central nervous system injury.  
XX  
XX Claim 89; Page 73; 200P; English.  
XX  
XX The invention relates to a nucleic acid molecule which down regulates  
XX expression of a CD20 gene and a nucleic acid molecule which down  
XX regulates expression of a neurite growth inhibitor gene (NCOG). The  
XX nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
XX DNazyme) an inozyme (an endolytic nucleic acid cleaving a RNA molecule  
XX possessing an NCH motif), a G-cleaver (cleaving RNA with a NTN motif) or  
XX an amberyne (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
XX with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
XX of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
XX Furthermore, it may be contacted with a cell to reduce CD20 activity of  
XX the cell and treat a patient having a condition associated with the level  
XX of CD20. The treatment may further comprise the use of one or more  
XX therapies. In particular, the CD20 targeting nucleic acid may be used to  
XX treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
XX Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
XX leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
XX lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
XX immune thrombocytopenia, and inflammatory arthropathy. The NCOG-

CC targeting nucleic acid is used to cleave RNA of the NCOG gene in the  
CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
CC nucleic acid may be contacted with a cell to reduce NCOG activity of the  
CC cell and treat a patient having a condition associated with the level of  
CC NCOG. The treatment may further comprise the use of one or more  
CC therapies. In particular, the NCOG-targeting nucleic acid may be used to  
CC treat central nervous system (CNS) injury and cerebrovascular accident  
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
CC disease, muscular dystrophy, and/or other neurodegenerative disease  
CC states which respond to the modulation of NCOG expression. The present  
CC sequence is a substrate sequence for a nucleic acid of the invention  
CC based on the human NCOG sequence  
XX  
SQ Sequence 38 BP; 11 A; 9 C; 13 G; 0 T; 5 U; 0 Other;  
XX  
Query Match 78.4%; Score 29.8; DB 4; Length 38;  
Best Local Similarity 93.9%; Pred. No. 0.0032;  
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
OY 4 GCAUUCUGAGGCGGUAGGCCGAAAAAUCA 36  
DB 4 GCAUUCUGAGGCGGUAGGCCGAAAAAGACA 36  
XX  
RESULT 33  
ABK04122  
ID ABK04122 standard; RNA; 38 BP.  
XX  
XX ABK04122;  
XX  
XX 12-MAR-2002 (first entry)  
XX  
XX Human NCOG Hammerhead ribozyme substrate sequence #329.  
XX  
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
XX cerebrioprotective; neurotropic; neuroprotective; antiparkinsonian;  
XX muscular; CD20; neurite growth inhibitor gene; NCOG; hammerhead ribozyme;  
XX DNazyme; inozyme; G-cleaver; amberyne; zinzyme; lymphoma; leukaemia;  
XX B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
XX human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
XX MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
XX inflammatory arthropathy; central nervous system injury;  
XX cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
XX chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
XX Parkinson's disease; ataxia; Huntington's disease; substrate sequence;  
XX Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
XX  
XX Homo sapiens.  
XX Synthetic.  
XX WO200159103-A2.  
XX  
XX 16-AUG-2001.  
XX  
XX 09-FEB-2001; 2001WO-US004273.  
XX  
XX 11-FEB-2000; 2000US-0181797P.  
XX 28-FEB-2000; 2000US-0185516P.  
XX 06-MAR-2000; 2000US-0187128P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX (BLAT/) BLATT L.  
XX (MCSW/) MCSWIGGEN J.  
XX (CHOW/) CHOWRIRA B M.  
XX  
XX Blatt L, Mcswiggen J, Chowrira BM;  
XX WPI; 2001-607195/69.  
XX  
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
XX constructs, which down regulate expression of a CD20 gene or neurite



```
ACN26108
ID ACN26108 standard; RNA; 38 BP.
XX
XX ACN26108;
AC
XX
XX 22-APR-2004 (first entry)
DT
XX
XX MNV minus strand Hammerhead Ribozyme SEQ ID NO 26124.
DE
XX
XX MNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX vircicide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
OS
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGEN J A.
XX
XX Blatt L, Mcswigen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (MNV), useful for treating a condition related to MNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 24; SEQ ID NO 26124; 495bp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (MNV). The nucleic acid molecules are useful for
XX treating a condition related to MNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention.
XX
XX Sequence 38 BP; 13 A; 7 C; 13 G; 0 T; 5 U; 0 Other;
SQ
XX
XX Query Match 78.4%; Score 29.8; DB 6; Length 38;
XX Best Local Similarity 93.9%; Pred. No. 0.0032;
XX Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 6 AAUTCUGAUGAGGCCGUTUAGGCCGAAAUUUCAG 38
DB 6 AAATCUGAUGAGGCCGUTUAGGCCGAAAUUUCAG 38
XX
XX
XX RESULT 36
XX ACN27859
ID ACN27859 standard; RNA; 38 BP.
XX
XX ACN27859;
AC
XX
XX 22-APR-2004 (first entry)
DT
XX
```

```
DE
XX
XX MNV minus strand Hammerhead Ribozyme SEQ ID NO 27875.
XX
XX MNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX vircicide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
OS
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGEN J A.
XX
XX Blatt L, Mcswigen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (MNV), useful for treating a condition related to MNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 24; SEQ ID NO 27875; 495bp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (MNV). The nucleic acid molecules are useful for
XX treating a condition related to MNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention.
XX
XX Sequence 38 BP; 14 A; 9 C; 9 G; 0 T; 6 U; 0 Other;
SQ
XX
XX Query Match 78.4%; Score 29.8; DB 6; Length 38;
XX Best Local Similarity 93.9%; Pred. No. 0.0032;
XX Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 5 CAUUCUGAUGAGGCCGUTUAGGCCGAAAUUUCAG 37
DB 5 CAUUCUGAUGAGGCCGUTUAGGCCGAAAUUUCAG 37
XX
XX
XX RESULT 37
XX ACD50588
ID ACD50588 standard; RNA; 38 BP.
XX
XX ACD50588;
AC
XX
XX 23-SEP-2003 (first entry)
DT
XX
XX HBV hammerhead ribozyme sequence #105.
XX
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNazyme; Inozyme; Zinzyme;
XX amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer I region; viral replication;
```

KW degenerative, disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW vincristine; antiinflammatory; ss.

OS Hepatitis B virus.

PN WO200281494-A1.

PD 17-OCT-2002.

PF 26-MAR-2002; 2002WO-US009187.

PR 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-0087478.

PR 08-JUN-2001; 2001US-0296876P.

PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.

PA (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MACE/) MACEJAK D.

PA (MCSW/) MCSWIGEN J.

PA (MORR/) MORRISSEY D.

PA (PACV/) PAVCO P.

PA (LEBP/) LEE P.

PA (DRAP/) DRAPER K.

PA (ROBE/) ROBERTS E.

PI Blatt L, Macejak D, Mcswigen J, Morrissey D, Pavco P, Lee P,

PI Draper K, Roberts E;

DR WPI; 2003-229207/22.

XX Novel compound useful for treating cirrhosis, liver failure,

XX hepatocellular carcinoma, or condition associated with hepatitis C virus

XX infection.

XX Example 1; Page 138; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate

XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or

XX Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense

XX and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,

XX inozymes, zinczymes, amberyzymes, and G-cleaver ribozymes. Also disclosed

XX are nucleic acid decoy molecules and aptamers that bind to HBV reverse

XX transcriptase and/or HBV reverse transcriptase primer sequences, as well

XX as oligonucleotides that specifically bind the Enhancer 1 region of HBV

XX DNA. The nucleic acids may be used to modulate the expression of HBV

XX genes and HBV viral replication. Also disclosed is a method for screening

XX compounds and/or potential therapies directed against HBV. The compounds

XX that modulate the expression and/or replication of HCV, the compounds and

XX methods of the invention are useful for the treatment of degenerative and

XX disease states related to HBV and HCV infection, replication and gene

XX expression such as cirrhosis, liver failure, and hepatocellular

XX carcinoma. The present sequence represents one of the HBV ribozyme,

XX inozyme, G-cleaver, zinczyme, DNazyme or amberyzyme sequences disclosed in

XX the present invention

XX

XX

XX

XX

AC ADL56345;

XX 20-MAY-2004 (first entry)

XX Human PKR ribozyme sequence #809.

XX antisense oligonucleotide; neurite growth inhibitor; NOGO;

XX prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;

XX protein kinase PKR; cerebrovascular accident;

XX central nervous system injury; CNS injury; spinal cord injury; cancer;

XX melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

XX restenosis; asthma; Crohn's disease; diabetes; obesity;

XX autoimmune disease; lupus; multiple sclerosis; transplant rejection;

XX graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;

XX allergy; asthma; allergic rhinitis; atopic dermatitis; PKR ribozyme;

XX substrate; ss; human.

XX Homo sapiens.

XX WO200281628-A2.

XX 17-OCT-2002.

XX 03-APR-2002; 2002WO-US010512.

XX 05-APR-2001; 2001US-00827395.

XX 29-MAY-2001; 2001US-0294412P.

XX 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;

XX WPI; 2003-058513/05.

XX Novel enzymatic nucleic acid that down-regulates expression of neurite

XX growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or

XX protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 57; SEQ ID NO 9878; 317pp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)

XX that down regulate the expression or inhibit the function of a receptor

XX for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),

XX Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the

XX invention are useful for treating: cerebrovascular accident, central

XX nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,

XX lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,

XX restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune

XX disease, lupus, multiple sclerosis, transplant/graft rejection,

XX ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic

XX conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The

XX nucleic acids of the invention are also useful for down-regulating the

XX expression of a target gene and as a diagnostic tool to examine genetic

XX defects and mutations within diseased cells or to detect the presence of a

XX target RNA in a cell. The present RNA sequence represents a human PKR

XX ribozyme sequence.

XX

XX

XX

XX

Query Match 78.4%; Score 29.8; DB 8; Length 38;  
 Best Local Similarity 93.9%; Pred. No. 0.0032;  
 Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCUGCAUUCUGAUGAGCCGUTAGCCGAAAAA 33  
 |||||  
 DB 1 CCUGGAUUCUGAUGAGCCGUTAGCCGAAAAA 33

RESULT 38  
 ADL56345  
 ID ADL56345 standard; RNA; 38 BP.  
 XX

Query Match 78.4%; Score 29.8; DB 11; Length 38;  
 Best Local Similarity 91.2%; Pred. No. 0.0032;  
 Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCAUUCUGAUGAGCCGUTAGCCGAAAAAUCAG 37  
 |||||  
 DB 4 GCAAAUCUGAUGAGCCGUTAGCCGAAAAAACAG 37

RESULT 39  
 ADM60513  
 ID ADM60513 standard; RNA; 38 BP.  
 XX

AC ADM60513;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Hepatitis B virus (HBV) enzymatic nucleic acid #105.  
 XX  
 KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;  
 KW Hepatitis B virus infection; hepatitis; hepatocellular carcinoma;  
 KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;  
 KW virucide; hepatotropic; antiinflammatory; cytosstatic.  
 XX  
 OS Hepatitis B virus.  
 XX  
 PN US2004054156-A1.  
 XX  
 PD 18-MAR-2004.  
 XX  
 PF 15-JAN-2003; 2003US-00342902.  
 XX  
 PR 14-MAY-1992; 92US-00882712.  
 PR 07-FEB-1994; 94US-00193627.  
 PR 08-NOV-1999; 99US-00436430.  
 PR 20-MAR-2000; 2000US-00531025.  
 PR 09-AUG-2000; 2000US-00636385.  
 PR 24-OCT-2000; 2000US-00696347.  
 PR 08-JUN-2001; 2001US-00877478.  
 XX  
 PA (DRAP/) DRAPER K.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 PA (MORR/) MORRISSEY D.  
 XX  
 PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;  
 DR  
 DR WPI: 2004-247781/23.  
 XX  
 PT Novel enzymatic nucleic acid molecule such as DNazymes and inozymes  
 PT specifically cleaving RNA derived from hepatitis B virus and comprising  
 PT one or more binding arms, useful for treating hepatitis and cirrhosis.  
 XX  
 PS Disclosure; SEQ ID NO 2647; 122bp; English.  
 XX  
 CC The invention relates to an enzymatic nucleic acid molecule that  
 CC specifically cleaves RNA derived from hepatitis B virus (HBV) and  
 CC comprising one or more binding arms, without requiring the presence of a  
 CC 2'-OH group within the molecule for activity. The nucleic acids are  
 CC useful for treating hepatitis B virus infection, hepatitis,  
 CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in  
 CC combination with other therapies such as lamivudine and interferons. The  
 CC nucleic acids are useful as diagnostic tools to examine genetic drift and  
 CC mutations within diseased cells, for detecting the presence of HBV RNA in  
 CC a cell, for the study of RNA and for down-regulating gene expression of  
 CC target genes in bacterial, fungal, viral, plant or mammalian cells. This  
 CC sequence represents an enzymatic nucleic acid molecule which cleaves HBV  
 CC RNA of the invention. Note: The sequence data for this patent is also  
 CC available in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 CC  
 SQ Sequence 38 BP; 11 A; 8 C; 13 G; 0 T; 6 U; 0 Other;  
 XX  
 XX  
 Query Match 78.4%; Score 29.8; DB 12; Length 38;  
 Best Local Similarity 93.9%; Pred. No. 0.0032;  
 Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CCUGCAUCUGAUGAGCGCGUAGGCCGAAAAA 33  
 DB 1 CCUGCAUCUGAUGAGCGCGUAGGCCGAAAAA 33  
 RESULT 40  
 ABX02648  
 ID ABX02648 standard; RNA; 36 BP.

AC ABX02648;  
 XX  
 DT 23-DEC-2002 (first entry)  
 XX  
 DE HCV hammerhead ribozyme #821 for Hepatitis C virus substrate #821.  
 XX  
 KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;  
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;  
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;  
 KW type I interferon; interferon alpha; interferon beta; cytosstatic;  
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;  
 KW hammerhead ribozyme; HH ribozyme; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN US2002082225-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PR 23-MAR-1999; 99US-00274553.  
 XX  
 PR 23-MAR-1999; 99US-00274553.  
 XX  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 PA (ROBE/) ROBERTS B.  
 PA (PAVC/) PAVCO P A.  
 PA (MACE/) MACEJACK D.  
 XX  
 PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;  
 DR  
 DR WPI: 2002-617759/66.  
 XX  
 PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral  
 PT replication and are useful to treat hepatitis C virus infections and  
 PT cirrhosis, liver failure or hepatocellular carcinoma.  
 XX  
 PS Claim 8; Page 45; 80bp; English.  
 XX  
 CC The present invention relates to enzymatic nucleic acids which  
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The  
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin  
 CC (HP) motif where the binding arms comprise sequences complementary to one  
 CC of the substrate sequences defined in the specification. The HCV  
 CC ribozymes are useful for modulating the expression and/or replication of  
 CC HCV. They can be used to treat cirrhosis, liver failure and/or  
 CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating  
 CC a condition associated with HCV infection in conjunction with one or more  
 CC other drug therapies, particularly type I interferon, especially  
 CC interferon alpha, beta or gamma or consensus interferon. The present  
 CC sequence represents a HCV hammerhead (HH) ribozyme. Note: Some of the  
 CC sequence data for this patent did not form part of the printed  
 CC specification. The complete sequence data for this patent was obtained in  
 CC electronic format directly from the USPTO web site at  
 CC seqdata.uspto.gov/patidentry.html  
 CC  
 SQ Sequence 36 BP; 9 A; 9 C; 12 G; 0 T; 6 U; 0 Other;  
 XX  
 XX  
 Query Match 77.9%; Score 29.6; DB 6; Length 36;  
 Best Local Similarity 88.9%; Pred. No. 0.0039;  
 Matches 32; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 CUGCAUCUGAUGAGCGCGUAGGCCGAAAAAUCAG 37  
 DB 1 CCGCAUCUGAUGAGCGCGUAGGCCGAAACGUCAG 36  
 Search completed: May 13, 2005, 17:06:07  
 Job time : 282.173 secs



## ALIGNMENTS

RESULT 1  
US-09-371-772B-8898/ Sequence 8898, Application US/09371772B  
/ Patent No. 6566127

/ GENERAL INFORMATION:

/ APPLICANT: Ribozyme Pharmaceuticals, Inc.

/ APPLICANT: Pavco, Pam

/ APPLICANT: McSwigen, Jim

/ APPLICANT: Stinchcomb, Dan

/ APPLICANT: Escobedo, Jaime

/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor

/ FILE REFERENCE: MBH00,876-J (237/198)

/ CURRENT APPLICATION NUMBER: US/09/371,772B

/ PRIOR FILING DATE: 1999-08-10

/ PRIOR APPLICATION NUMBER: US 60/005,974

/ PRIOR FILING DATE: 1995-10-26

/ PRIOR APPLICATION NUMBER: US 08/584,040

/ NUMBER OF SEQ ID NOS: 14225

/ SOFTWARE: PatentIn version 3.0

/ SEQ ID NO 8898

/ LENGTH: 38

/ TYPE: RNA

/ ORGANISM: Artificial Sequence

/ FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-371-772B-8898

Query Match  
Best Local Similarity 82.1%; Score 31.2; DB 4; Length 38;  
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;QY 1 CCUGCAUCUGAUGAGCGCCGUUAGCGCGAAGAAUUA 36  
DB 1 CCUCACAUUCUGAUGAGCGCCGUUAGCGCGAAGAAUUA 36RESULT 2  
US-09-371-772B-9385

/ Sequence 9385, Application US/09371772B

/ Patent No. 6566127

/ GENERAL INFORMATION:

/ APPLICANT: Ribozyme Pharmaceuticals, Inc.

/ APPLICANT: Pavco, Pam

/ APPLICANT: McSwigen, Jim

/ APPLICANT: Stinchcomb, Dan

/ APPLICANT: Escobedo, Jaime

/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor

/ FILE REFERENCE: MBH00,876-J (237/198)

/ CURRENT APPLICATION NUMBER: US/09/371,772B

/ PRIOR FILING DATE: 1999-08-10

/ PRIOR APPLICATION NUMBER: US 60/005,974

/ PRIOR FILING DATE: 1995-10-26

/ PRIOR APPLICATION NUMBER: US 08/584,040

/ NUMBER OF SEQ ID NOS: 14225

/ SOFTWARE: PatentIn version 3.0

/ SEQ ID NO 9385

/ LENGTH: 38

/ TYPE: RNA

/ ORGANISM: Artificial Sequence

/ FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-371-772B-9385

Query Match 82.1%; Score 31.2; DB 4; Length 38;

Best Local Similarity 91.7%; Pred. No. 4.9e-05;  
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;QY 1 CCUGCAUCUGAUGAGCGCCGUUAGCGCGAAGAAUUA 36  
DB 1 CCUGCAUCUGAUGAGCGCCGUUAGCGCGAAGAAUUA 36RESULT 3  
US-09-371-772B-7472

/ Sequence 7472, Application US/09371772B

/ Patent No. 6566127

/ GENERAL INFORMATION:

/ APPLICANT: Ribozyme Pharmaceuticals, Inc.

/ APPLICANT: Pavco, Pam

/ APPLICANT: McSwigen, Jim

/ APPLICANT: Stinchcomb, Dan

/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor

/ FILE REFERENCE: MBH00,876-J (237/198)

/ CURRENT APPLICATION NUMBER: US/09/371,772B

/ PRIOR FILING DATE: 1999-08-10

/ PRIOR APPLICATION NUMBER: US 60/005,974

/ PRIOR FILING DATE: 1995-10-26

/ PRIOR APPLICATION NUMBER: US 08/584,040

/ NUMBER OF SEQ ID NOS: 14225

/ SOFTWARE: PatentIn version 3.0

/ SEQ ID NO 7472

/ LENGTH: 38

/ TYPE: RNA

/ ORGANISM: Artificial Sequence

/ FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-371-772B-7472

Query Match  
Best Local Similarity 81.1%; Score 30.8; DB 4; Length 38;  
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;QY 2 CUGCAUCUGAUGAGCGCCGUUAGCGCGAAGAAUUA 35  
DB 2 CCGCAGUCUGAUGAGCGCCGUUAGCGCGAAGAAUUA 35RESULT 4  
US-09-371-772B-8673

/ Sequence 8673, Application US/09371772B

/ Patent No. 6566127

/ GENERAL INFORMATION:

/ APPLICANT: Ribozyme Pharmaceuticals, Inc.

/ APPLICANT: Pavco, Pam

/ APPLICANT: McSwigen, Jim

/ APPLICANT: Stinchcomb, Dan

/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor

/ FILE REFERENCE: MBH00,876-J (237/198)

/ CURRENT APPLICATION NUMBER: US/09/371,772B

/ PRIOR FILING DATE: 1999-08-10

/ PRIOR APPLICATION NUMBER: US 60/005,974

/ PRIOR FILING DATE: 1995-10-26

/ PRIOR APPLICATION NUMBER: US 08/584,040

/ NUMBER OF SEQ ID NOS: 14225

/ SOFTWARE: PatentIn version 3.0

/ SEQ ID NO 8673

/ LENGTH: 38

/ TYPE: RNA

/ ORGANISM: Artificial Sequence

/ FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-371-772B-8673

Query Match 81.1%; Score 30.8; DB 4; Length 38;  
Best Local Similarity 94.1%; Pred. No. 7.5e-05;  
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCUGCAUUCGAGGCGGUAGGCCGAAAUU 34  
DB 1 CCUGCAUUCGAGGCGGUAGGCCGAAAUU 34

RESULT 5

US-09-371-772B-9574  
Sequence 9574, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyne Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwigen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Endothelial Cells  
FILE REFERENCE: MBH00, 876-J (237/198)  
CURRENT APPLICATION NUMBER: US/09/371, 772B  
CURRENT FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: US 60/005, 974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584, 040  
PRIOR FILING DATE: 1996-01-08  
NUMBER OF SEQ ID NOS: 14225  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 9574  
LENGTH: 38  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-9574

Query Match 80.5%; Score 30.6; DB 4; Length 38;  
Best Local Similarity 89.2%; Pred. No. 9.3e-05;  
Matches 33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CUGCAUUCGAGGCGGUAGGCCGAAAUU 38  
DB 2 CUGCAUUCGAGGCGGUAGGCCGAAAUU 38

RESULT 6

US-09-371-772B-9413  
Sequence 9413, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyne Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwigen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Endothelial Cells  
FILE REFERENCE: MBH00, 876-J (237/198)  
CURRENT APPLICATION NUMBER: US/09/371, 772B  
CURRENT FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: US 60/005, 974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584, 040  
PRIOR FILING DATE: 1996-01-08  
NUMBER OF SEQ ID NOS: 14225  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 9413  
LENGTH: 38  
TYPE: RNA

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-9413

Query Match 80.0%; Score 30.4; DB 4; Length 38;  
Best Local Similarity 96.9%; Pred. No. 0.00012;  
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCUGCAUUCGAGGCGGUAGGCCGAAAU 32  
DB 1 CCUGCAUUCGAGGCGGUAGGCCGAAAU 32

RESULT 7

US-09-371-772B-10563  
Sequence 10563, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyne Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwigen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Endothelial Cells  
FILE REFERENCE: MBH00, 876-J (237/198)  
CURRENT APPLICATION NUMBER: US/09/371, 772B  
CURRENT FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: US 60/005, 974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584, 040  
PRIOR FILING DATE: 1996-01-08  
NUMBER OF SEQ ID NOS: 14225  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 10563  
LENGTH: 38  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-10563

Query Match 80.0%; Score 30.4; DB 4; Length 38;  
Best Local Similarity 96.9%; Pred. No. 0.00012;  
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 AUCUGAUGAGGCGGUAGGCCGAAAUU 38  
DB 7 AUCUGAUGAGGCGGUAGGCCGAAAUU 38

RESULT 8

US-09-371-772B-8143  
Sequence 8143, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyne Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwigen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Endothelial Cells  
FILE REFERENCE: MBH00, 876-J (237/198)  
CURRENT APPLICATION NUMBER: US/09/371, 772B  
CURRENT FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: US 60/005, 974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584, 040  
PRIOR FILING DATE: 1996-01-08  
NUMBER OF SEQ ID NOS: 14225  
SOFTWARE: Patentin version 3.0

```

; SEQ ID NO 8143
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-371-772B-8143
```

```

Query Match
Best Local Similarity 79.5%; Score 30.2; DB 4; Length 38;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

QY 2 CCUGCAUUCGUAUGAGCCCGUUGAGCCGGAUUAUUA 36
Db 2 CUACAGUCGUAUGAGCCCGUUGAGCCGGAUUAUUA 36
```

## RESULT 9

```

US-09-371-772B-7526
; Sequence 7526, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7526
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-371-772B-7526
```

```

Query Match
Best Local Similarity 78.9%; Score 30; DB 4; Length 38;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```

QY 1 CCUGCAUUCGUAUGAGCCCGUUGAGCCGGAUUAUUA 38
Db 1 CCUAAAUUCGUAUGAGCCCGUUGAGCCGGAUUAUUA 38
```

## RESULT 10

```

US-09-371-772B-7766
; Sequence 7766, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; CURRENT APPLICATION NUMBER: US 08/584,040
```

```

; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7766
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-371-772B-7766
```

```

Query Match
Best Local Similarity 78.9%; Score 30; DB 4; Length 38;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```

QY 1 CCUGCAUUCGUAUGAGCCCGUUGAGCCGGAUUAUUA 38
Db 1 CCUGAAUUCGUAUGAGCCCGUUGAGCCGGAUUAUUA 38
```

## RESULT 11

```

US-09-371-772B-9539
; Sequence 9539, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9539
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-371-772B-9539
```

```

Query Match
Best Local Similarity 78.9%; Score 30; DB 4; Length 38;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 4 GCAUUCGUAUGAGCCCGUUGAGCCGGAUUAUUA 33
Db 4 GCAUUCGUAUGAGCCCGUUGAGCCGGAUUAUUA 33
```

## RESULT 12

```

US-09-371-772B-8240
; Sequence 8240, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; PRIOR FILING DATE: 1999-08-10
```

```

; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8240
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-371-772B-8240

Query Match      78.4%; Score 29.8; DB 4; Length 38;
Best Local Similarity 93.9%; Pred. No. 0.00022;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6 AAUCUGAUGAGGCCGUAAGCCGAAAAAUCAG 38
Db      6 AUUCUGAUGAGGCCGUAAGCCGAAAAAUCAG 38

RESULT 13
; Sequence 8345, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371, 772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8345
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-371-772B-8345

Query Match      78.4%; Score 29.8; DB 4; Length 38;
Best Local Similarity 93.9%; Pred. No. 0.00022;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6 AAUCUGAUGAGGCCGUAAGCCGAAAAAUCAG 38
Db      6 AUUCUGAUGAGGCCGUAAGCCGAAAAAUCAG 38

RESULT 14
; Sequence 8530, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
```

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; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371, 772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8530
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-371-772B-8530

Query Match      78.4%; Score 29.8; DB 4; Length 38;
Best Local Similarity 93.9%; Pred. No. 0.00022;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CCUGAAUUCUGAUGAGGCCGUAAGCCGAAAAAU 34
Db      2 CUGAAAUUCUGAUGAGGCCGUAAGCCGAAAAAU 34

RESULT 15
; Sequence 8913, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371, 772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8913
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-371-772B-8913

Query Match      77.9%; Score 29.6; DB 4; Length 38;
Best Local Similarity 88.9%; Pred. No. 0.00027;
Matches 32; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CCUGAAUUCUGAUGAGGCCGUAAGCCGAAAAUCA 36
Db      1 CGUGAAGCUGAUGAGGCCGUAAGCCGAAAAUCA 36

RESULT 16
; Sequence 7656, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
```

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; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; PRIORITY FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 7656
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-7656
```

```

Query Match          77.4%; Score 29.4; DB 4; Length 38;
Best Local Similarity 96.8%; Pred. No. 0.00034;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 7 AUCUGAUGAGCGCCGUAAGCCGCAAAAUAUCAG 37
DB 7 AACUGAUGAGCGCCGUAAGCCGCAAAAUAUCAG 37
```

```

RESULT 17
US-09-371-772B-7863
; Sequence 7863, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; PRIORITY FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 7863
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-7863
```

```

Query Match          77.4%; Score 29.4; DB 4; Length 38;
Best Local Similarity 96.8%; Pred. No. 0.00034;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 6 AAUCUGAUGAGCGCCGUAAGCCGCAAAAUAUCA 36
DB 6 AAACUGAUGAGCGCCGUAAGCCGCAAAAUAUCA 36
```

```

RESULT 18
US-09-371-772B-8422
; Sequence 8422, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

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; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; PRIORITY FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 8422
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8422
```

```

Query Match          77.4%; Score 29.4; DB 4; Length 38;
Best Local Similarity 96.8%; Pred. No. 0.00034;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 7 AUCUGAUGAGCGCCGUAAGCCGCAAAAUAUCAG 37
DB 7 AACUGAUGAGCGCCGUAAGCCGCAAAAUAUCAG 37
```

```

RESULT 19
US-09-371-772B-8953
; Sequence 8953, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; PRIORITY FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 8953
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8953
```

```

Query Match          77.4%; Score 29.4; DB 4; Length 38;
Best Local Similarity 96.8%; Pred. No. 0.00034;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 CCUGCAUCUGAUGAGCGCCGUAAGCCGCAAAA 31
DB 1 CCUGCAAGCUGAUGAGCGCCGUAAGCCGCAAAA 31
```

```

RESULT 20
US-09-371-772B-9507
; Sequence 9507, Application US/09371772B
```

Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwigen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
FILE REFERENCE: MBH00,876-J (237/198)  
CURRENT APPLICATION NUMBER: US/09/371,772B  
CURRENT FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: US 60/005,974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584,040  
PRIOR FILING DATE: 1996-01-08  
NUMBER OF SEQ ID NOS: 14225  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 9507  
LENGTH: 38  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-9507

Query Match 77.4%; Score 29.4; DB 4; Length 38;  
Best Local Similarity 96.8%; Pred. No. 0.00034;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 UCUGAUGAGCGCGUUGAGCGGAAAAUUCAGG 38  
Db 8 UCUGAUGAGCGCGUUGAGCGGAAAAUUCAGG 38

RESULT 21  
US-09-371-772B-9559  
Sequence 9559, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwigen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
FILE REFERENCE: MBH00,876-J (237/198)  
CURRENT APPLICATION NUMBER: US/09/371,772B  
CURRENT FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: US 60/005,974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584,040  
PRIOR FILING DATE: 1996-01-08  
NUMBER OF SEQ ID NOS: 14225  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 9559  
LENGTH: 38  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-9559

Query Match 77.4%; Score 29.4; DB 4; Length 38;  
Best Local Similarity 96.8%; Pred. No. 0.00034;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 UCUGAUGAGCGCGUUGAGCGGAAAAUUCAGG 38  
Db 8 UCUGAUGAGCGCGUUGAGCGGAAAAUUCAGG 38

RESULT 22  
US-09-371-772B-11300  
Sequence 11300, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwigen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
FILE REFERENCE: MBH00,876-J (237/198)  
CURRENT APPLICATION NUMBER: US/09/371,772B  
CURRENT FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: US 60/005,974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584,040  
PRIOR FILING DATE: 1996-01-08  
NUMBER OF SEQ ID NOS: 14225  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 11300  
LENGTH: 38  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
NAME/KEY: misc feature  
LOCATION: (31)..(31)  
OTHER INFORMATION: n stands for inosine  
US-09-371-772B-11300

Query Match 77.4%; Score 29.4; DB 4; Length 38;  
Best Local Similarity 93.8%; Pred. No. 0.00034;  
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCUGCAUUCUGAUGAGCGCGUUGAGCGGAAAA 32  
Db 1 CCUGCAUUCUGAUGAGCGCGUUGAGCGGAAAA 32

RESULT 23  
US-08-373-124A-1754  
Sequence 1754, Application US/08373124A  
Patent No. 5646042  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Draper, Kenneth  
APPLICANT: McSwigen, James  
APPLICANT: Jarvis, Thale  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TITLE OF INVENTION: TREATMENT OF RESPIRATORY AND  
TITLE OF INVENTION: CANCER USING RIBOZYMES  
NUMBER OF SEQUENCES: 2627  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/373,124A  
FILING DATE: January 13, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994  
APPLICATION NUMBER: 08/192,943  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: 07/987,132  
FILING DATE: December 7, 1992  
APPLICATION NUMBER: 07/936,422  
FILING DATE: August 26, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/035  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1754:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-373-124A-1754

Query Match: 76.8%; Score 29.2; DB 1; Length 38;  
Best Local Similarity 91.2%; Pred. No. 0.00042;  
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CAUUCUGAUGAGCGCCGUAAGCCGAAAUUUCAG 38  
Db 5 CAUUCUGAUGAGCGCCGUAAGCCGAAAUUUCAG 38

RESULT 24  
US-08-435-628-1754  
Sequence 1754, Application US/08435628  
Patent No. 5817796  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Draper, Kenneth  
APPLICANT: McSwiggen, James  
APPLICANT: Jarvis, Thale  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND  
NUMBER OF SEQUENCES: 2627  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,628  
FILING DATE: 05-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/373,124  
FILING DATE: January 13, 1995  
APPLICATION NUMBER: 08/245,466  
FILING DATE: May 18, 1994  
APPLICATION NUMBER: 08/192,943  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: 07/987,132  
FILING DATE: December 7, 1992  
APPLICATION NUMBER: 07/936,422

FILING DATE: August 26, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/035  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1754:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-435-628-1754

Query Match: 76.8%; Score 29.2; DB 1; Length 38;  
Best Local Similarity 91.2%; Pred. No. 0.00042;  
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CAUUCUGAUGAGCGCCGUAAGCCGAAAUUUCAG 38  
Db 5 CAUUCUGAUGAGCGCCGUAAGCCGAAAUUUCAG 38

RESULT 25  
US-09-371-772B-8298  
Sequence 8298, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Becabeco, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel  
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: MBH00,876-J (237/198)  
CURRENT APPLICATION NUMBER: US/09/371,772B  
CURRENT FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: US 60/005,974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584,040  
PRIOR FILING DATE: 1996-01-08  
NUMBER OF SEQ ID NOS: 14225  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 8298  
LENGTH: 38  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-8298

Query Match: 76.8%; Score 29.2; DB 4; Length 38;  
Best Local Similarity 91.2%; Pred. No. 0.00042;  
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CAUUCUGAUGAGCGCCGUAAGCCGAAAUUUCAG 38  
Db 5 CAUUCUGAUGAGCGCCGUAAGCCGAAAUUUCAG 38

RESULT 26  
US-09-371-772B-8707  
Sequence 8707, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan

```

; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc

```

; Sequence 13264, Application US/09371772E

```
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MBH00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13264
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
LOCATION: (31)..(31)
OTHER INFORMATION: n stands for inosine
US-09-371-772B-13264
```

```
Query Match          76.3%; Score 29; DB 4; Length 38;
Best Local Similarity 96.7%; Pred. No. 0.00052;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 7 AUCUGAGGAGCGGUGAGCCGGAANAUA 36
Db 7 AUCUGAGGAGCGGUGAGCCGGAANAUA 36
```

```
RESULT 31
US-09-371-772B-7533
Sequence 7533, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MBH00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7533
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-7533
```

```
Query Match          75.8%; Score 28.8; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 0.00064;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 CCUGCAUUCUGAGGCGGUGAGCCGGAANA 32
Db 1 CCUGCAUUCUGAGGCGGUGAGCCGGAANA 32
```

```
Db 1 CUUUCAUUCUGAGGCGGUGAGCCGGAANA 32
```

```
RESULT 32
US-09-371-772B-8047
Sequence 8047, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MBH00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8047
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8047
```

```
Query Match          75.8%; Score 28.8; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 0.00064;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 5 CAUUCUGAGGAGCGGUGAGCCGGAANAUA 36
Db 5 CAUUCUGAGGAGCGGUGAGCCGGAANAUA 36
```

```
RESULT 33
US-09-371-772B-8328
Sequence 8328, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MBH00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8328
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8328
```

```
Query Match          75.8%; Score 28.8; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 0.00064;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 CCUGCAUCUGAUGAGCCGCUAGGCCGAAAA 32  
|||  
Db 1 CCUAAAUCUGAUGAGCCGCUAGGCCGAAAA 32

## RESULT 34

US-09-371-772B-10400  
; Sequence 10400, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00, 876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371, 772B  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005, 974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584, 040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10400  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-10400

Query Match 75.8%; Score 28.8; DB 4; Length 38;  
Best Local Similarity 93.8%; Pred. No. 0.00064;  
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 UGCAUCUGAUGAGCCGCUAGGCCGAAAAAU 34  
|||  
Db 3 UGCAUCUGAUGAGCCGCUAGGCCGAAAAAU 34

## RESULT 35

US-09-371-772B-10648  
; Sequence 10648, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00, 876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371, 772B  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005, 974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584, 040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10648  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-10648

Query Match 75.8%; Score 28.8; DB 4; Length 38;  
Best Local Similarity 93.8%; Pred. No. 0.00064;  
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCUGCAUCUGAUGAGCCGCUAGGCCGAAAA 33  
|||  
Db 2 CCUGCAUCUGAUGAGCCGCUAGGCCGAAAA 33

## RESULT 36

US-09-371-772B-11044  
; Sequence 11044, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00, 876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371, 772B  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005, 974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584, 040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 11044  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-11044

Query Match 75.8%; Score 28.8; DB 4; Length 38;  
Best Local Similarity 93.8%; Pred. No. 0.00064;  
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 MAUCUGAUGAGCCGCUAGGCCGAAAAAUCAG 37  
|||  
Db 6 MAUCUGAUGAGCCGCUAGGCCGAAAAAUCG 37

## RESULT 37

US-09-371-772B-12223  
; Sequence 12223, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00, 876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371, 772B  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005, 974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584, 040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12223  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-12223

OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
NAME/KEY: misc\_feature  
LOCATION: (31)..(31)  
NUMBER OF SEQ ID NOS: 14225  
OTHER INFORMATION: n stands for inosine  
US-09-371-772B-12223

Query Match 75.8%; Score 28.8; DB 4; Length 38;  
Best Local Similarity 90.9%; Pred. No. 0.00064;  
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CUGCAUUCUGAGAGCCGCUUAGCCGGAANAUCAG 34  
Db 2 CUGAAUUCUGAGAGCCGCUUAGCCGGAANAUC 34

RESULT 38  
US-09-371-772B-12495  
Sequence 12495, Application US/09371772B  
Patent No. 6566127

GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, Jim  
APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MBH00,876-J (237/198)

CURRENT APPLICATION NUMBER: US/09/371,772B

PRIOR FILING DATE: 1999-08-10

PRIOR APPLICATION NUMBER: US 60/005,974

PRIOR FILING DATE: 1995-10-26

PRIOR APPLICATION NUMBER: US 08/584,040

PRIOR FILING DATE: 1996-01-08

NUMBER OF SEQ ID NOS: 14225

SOFTWARE: PatentIn version 3.0

SEQ ID NO 12495

LENGTH: 38

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

NAME/KEY: misc\_feature

LOCATION: (31)..(31)

OTHER INFORMATION: n stands for inosine  
US-09-371-772B-12495

Query Match 75.8%; Score 28.8; DB 4; Length 38;  
Best Local Similarity 90.9%; Pred. No. 0.00064;  
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 AAUCUGAGAGCCGCUUAGCCGGAANAUCAG 38  
Db 6 AAUCUGAGAGCCGCUUAGCCGGAANAUCAG 38

RESULT 39  
US-09-371-772B-13894

Sequence 13894, Application US/09371772B  
Patent No. 6566127

GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, Jim

APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MBH00,876-J (237/198)

CURRENT APPLICATION NUMBER: US/09/371,772B

PRIOR FILING DATE: 1999-08-10

PRIOR APPLICATION NUMBER: US 60/005,974

PRIOR FILING DATE: 1995-10-26

PRIOR APPLICATION NUMBER: US 08/584,040  
PRIOR FILING DATE: 1996-01-08  
NUMBER OF SEQ ID NOS: 14225  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 13894

Query Match 75.8%; Score 28.8; DB 4; Length 38;  
Best Local Similarity 90.9%; Pred. No. 0.00064;  
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 AAUCUGAGAGCCGCUUAGCCGGAANAUCAG 38  
Db 6 AAUCUGAGAGCCGCUUAGCCGGAANAUCAG 38

RESULT 40  
US-09-371-772B-7626  
Sequence 7626, Application US/09371772B  
Patent No. 6566127

GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, Jim

APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MBH00,876-J (237/198)

CURRENT APPLICATION NUMBER: US/09/371,772B

PRIOR FILING DATE: 1999-08-10

PRIOR APPLICATION NUMBER: US 60/005,974

PRIOR FILING DATE: 1995-10-26

PRIOR APPLICATION NUMBER: US 08/584,040

PRIOR FILING DATE: 1996-01-08

NUMBER OF SEQ ID NOS: 14225

SOFTWARE: PatentIn version 3.0

SEQ ID NO 7626

LENGTH: 38

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

NAME/KEY: misc\_feature

LOCATION: (31)..(31)

OTHER INFORMATION: n stands for inosine  
US-09-371-772B-7626

Query Match 75.3%; Score 28.6; DB 4; Length 38;  
Best Local Similarity 88.6%; Pred. No. 0.0008;  
Matches 31; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 UGCAUUCUGAGAGCCGCUUAGCCGGAANAUCAG 37  
Db 3 UGCAUUCUGAGAGCCGCUUAGCCGGAANAUCAG 37

Search completed: May 13, 2005, 18:27:24  
Job time : 94.9636 secs



85	29.4	77.4	38	10	US-09-877-478-2776	Sequence 2776, Ap
86	29.4	77.4	38	10	US-09-848-754A-4943	Sequence 4943, Ap
87	29.4	77.4	38	10	US-09-930-423-1858	Sequence 1858, Ap
88	29.4	77.4	38	10	US-09-745-237A-1858	Sequence 1858, Ap
89	29.4	77.4	38	15	US-10-156-306-901	Sequence 901, App
90	29.4	77.4	38	15	US-10-156-306-2009	Sequence 2009, Ap
91	29.4	77.4	38	17	US-10-342-902-2776	Sequence 2776, Ap
92	29.4	77.4	38	17	US-10-138-674-9933	Sequence 9933, Ap
93	29.4	77.4	38	17	US-10-138-674-10140	Sequence 10140, A
94	29.4	77.4	38	17	US-10-138-674-10699	Sequence 10699, A
95	29.4	77.4	38	17	US-10-138-674-11230	Sequence 11230, A
96	29.4	77.4	38	17	US-10-138-674-11784	Sequence 11784, A
97	29.4	77.4	38	17	US-10-138-674-11836	Sequence 11836, A
98	29.4	77.4	38	17	US-10-138-674-13577	Sequence 13577, A
99	29.4	77.4	38	18	US-10-287-949A-9933	Sequence 9933, Ap
100	29.4	77.4	38	18	US-10-287-949A-10140	Sequence 10140, A

## ALIGNMENTS

RESULT 1  
US-09-927-046-2332

```

; Sequence 2332, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2332
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-927-046-2332

```

```

Query Match          100.0%; Score 38; DB 10; Length 38;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  CCUGCAUCUGAUGAGGCCGUGAGCCGGAAGAAUACAG 38
Db      1  CCUGCAUCUGAUGAGGCCGUGAGCCGGAAGAAUACAG 38

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RESULT 2  
US-09-927-046-5432

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; Sequence 5432, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046

```

```

; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5432
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

```

```

; LOCATION: (1) .. (4)
; NAME/KEY: misc_feature
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
; LOCATION: (1) .. (8)
; NAME/KEY: misc_feature
; OTHER INFORMATION: 2'-O-Methyl
; LOCATION: (12) .. (12)
; NAME/KEY: misc_feature
; OTHER INFORMATION: 2'-O-Methyl
; LOCATION: (14) .. (26)
; NAME/KEY: misc_feature
; OTHER INFORMATION: 2'-O-Methyl
; LOCATION: (28) .. (29)
; NAME/KEY: misc_feature
; OTHER INFORMATION: 2'-O-Methyl
; LOCATION: (31) .. (36)
; NAME/KEY: misc_feature
; OTHER INFORMATION: 2'-O-Methyl
; LOCATION: (9) .. (9)
; NAME/KEY: misc_feature
; OTHER INFORMATION: 2'-deoxy-2'-C-Allyl
; LOCATION: (37) .. (37)
; NAME/KEY: misc_feature
; OTHER INFORMATION: n stands for inverted deoxybasic derivative
US-09-927-046-5432

```

```

Query Match          94.7%; Score 36; DB 10; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2  CCUGCAUCUGAUGAGGCCGUGAGCCGGAAGAAUACAG 37
Db      1  CCUGCAUCUGAUGAGGCCGUGAGCCGGAAGAAUACAG 36

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RESULT 3  
US-09-780-533A-3045

```

; Sequence 3045, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3045
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-533A-3045

```

```

Query Match          83.7%; Score 31.8; DB 10; Length 38;
Best Local Similarity 94.3%; Pred. No. 0.00035;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy 2 CUGCAUCUGAUGAGCCGCUUAGGCCGAAAAAUAUC 36  
 |||  
 Db 2 CUUUAUUCUGAUGAGCCGCUUAGGCCGAAAAAUAUC 36

RESULT 4  
 US-09-848-754A-4217  
 ; Sequence 4217, Application US/09848754A  
 ; Publication No. US20030073207A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
 ; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
 ; FILE REFERENCE: MBH800-958-1 (400/018)  
 ; CURRENT APPLICATION NUMBER: US/09/848,754A  
 ; NUMBER OF SEQ ID NOS: 9645  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 4217  
 ; LENGTH: 38  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid  
 US-09-848-754A-4217

Query Match 83.7%; Score 31.8; DB 10; Length 38;  
 Best Local Similarity 94.3%; Pred. No. 0.00035;  
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CUGCAUCUGAUGAGCCGCUUAGGCCGAAAAAUAUC 36  
 |||  
 Db 2 CUUUAUUCUGAUGAGCCGCUUAGGCCGAAAAAUAUC 36

RESULT 5  
 US-09-780-533A-3244  
 ; Sequence 3244, Application US/09780533A  
 ; Publication No. US20030060611A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
 ; APPLICANT: Blatt, Larry  
 ; APPLICANT: McSwiggen, Jim  
 ; APPLICANT: Chowrira, Bharat  
 ; APPLICANT: Haeblerli, Pete  
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
 ; FILE REFERENCE: MBH800,878-A (400/011)  
 ; CURRENT APPLICATION NUMBER: US/09/780,533A  
 ; CURRENT FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: US 60/181,797  
 ; PRIOR FILING DATE: 2000-02-11  
 ; NUMBER OF SEQ ID NOS: 6679  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 3244  
 ; LENGTH: 38  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
 US-09-780-533A-3244

Query Match 82.6%; Score 31.4; DB 10; Length 38;  
 Best Local Similarity 97.0%; Pred. No. 0.00053;  
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CAUCUGAUGAGCCGCUUAGGCCGAAAAAUAUC 37  
 |||  
 Db 5 CAUCUGAUGAGCCGCUUAGGCCGAAAAAUAUC 37

RESULT 6  
 US-09-927-046-2304

; Sequence 2304, Application US/09927046  
 ; Publication No. US20030064946A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc  
 ; APPLICANT: McSwiggen, Jim  
 ; APPLICANT: Thompson, Jim  
 ; APPLICANT: McKenzie, Tim  
 ; APPLICANT: Ayers, Dave  
 ; APPLICANT: Grube, Andrew  
 ; APPLICANT: Szymkowski, Edmund  
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric  
 ; FILE REFERENCE: 249/021  
 ; CURRENT APPLICATION NUMBER: US/09/927,046  
 ; CURRENT FILING DATE: 2001-08-09  
 ; NUMBER OF SEQ ID NOS: 5450  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 2304  
 ; LENGTH: 38  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
 US-09-927-046-2304

Query Match 82.6%; Score 31.4; DB 10; Length 38;  
 Best Local Similarity 97.0%; Pred. No. 0.00053;  
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 UGAAUUCUGAUGAGCCGCUUAGGCCGAAAAAUAUC 35  
 |||  
 Db 3 UGAAUUCUGAUGAGCCGCUUAGGCCGAAAAAUAUC 35

RESULT 7  
 US-09-877-478-3796  
 ; Sequence 3796, Application US/09877478  
 ; Publication No. US20030068301A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
 ; APPLICANT: Draper, Kenneth  
 ; APPLICANT: Blatt, Larry  
 ; APPLICANT: McSwiggen, Jim  
 ; APPLICANT: Morrissey, Dave  
 ; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication  
 ; FILE REFERENCE: MBH800-845-H (400/029)  
 ; CURRENT APPLICATION NUMBER: US/09/877,478  
 ; CURRENT FILING DATE: 2001-12-31  
 ; PRIOR APPLICATION NUMBER: US 07/882,712  
 ; PRIOR FILING DATE: 1992-05-14  
 ; PRIOR APPLICATION NUMBER: US 09/531,025  
 ; PRIOR FILING DATE: 2000-03-20  
 ; PRIOR APPLICATION NUMBER: US 09/636,385  
 ; PRIOR FILING DATE: 2000-08-09  
 ; PRIOR APPLICATION NUMBER: US 09/696,347  
 ; PRIOR FILING DATE: 2000-10-24  
 ; PRIOR APPLICATION NUMBER: US 08/193,627  
 ; PRIOR FILING DATE: 1994-02-07  
 ; PRIOR APPLICATION NUMBER: US 08/433,993  
 ; PRIOR FILING DATE: 1995-05-04  
 ; PRIOR APPLICATION NUMBER: US 08/434,504  
 ; PRIOR FILING DATE: 1995-05-04  
 ; PRIOR APPLICATION NUMBER: US 09/436,430  
 ; PRIOR FILING DATE: 1999-11-08  
 ; NUMBER OF SEQ ID NOS: 6586  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 3796  
 ; LENGTH: 38  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
 NAME/KEY: misc\_feature

LOCATION: (31)..(31)  
OTHER INFORMATION: n stands for inosine  
US-09-877-478-3796

Query Match 82.6%; Score 31.4; DB 10; Length 38;  
Best Local Similarity 94.1%; Pred. No. 0.00053;  
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCUGCAUCGAGUGAGCCGCUUAGGCCGAAAUU 34  
Db 1 CCUGCAACUGAGUGAGCCGCUUAGGCCGAAAUU 34

RESULT 8  
US-09-792-818-954

Sequence 954, Application US/09792818  
Publication No. US20030134806A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Jarvis, Thale

APPLICANT: Von Carlowitz, Ira

APPLICANT: McSwiggen, Jim

APPLICANT: Hamblin, Paul

APPLICANT: Ellis, Jonathan

TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse

FILE REFERENCE: MBH00-901-A (400/013)

CURRENT APPLICATION NUMBER: US/09/792,818

CURRENT FILING DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 2304

SOFTWARE: PatentIn version 3.0

SEQ ID NO 954

LENGTH: 38

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-792-818-954

Query Match 82.6%; Score 31.4; DB 10; Length 38;  
Best Local Similarity 97.0%; Pred. No. 0.00053;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCAUUCGAGUGAGCCGCUUAGGCCGAAAUU 36  
Db 4 GCAGUCGAGUGAGCCGCUUAGGCCGAAAUU 36

RESULT 9

US-10-342-902-3796

Sequence 3796, Application US/10342902

Publication No. US20040054156A1

GENERAL INFORMATION:

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Draper, Kenneth

APPLICANT: Blact, Larry

APPLICANT: McSwiggen, Jim

APPLICANT: Morrissey, Dave

TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication

FILE REFERENCE: 400/075 (MBH00-845-1)

CURRENT APPLICATION NUMBER: US/10/342,902

CURRENT FILING DATE: 2003-01-15

PRIOR APPLICATION NUMBER: US 09/877,478

PRIOR FILING DATE: 2001-06-08

PRIOR APPLICATION NUMBER: US 09/531,025

PRIOR FILING DATE: 2000-03-20

PRIOR APPLICATION NUMBER: US 09/636,385

PRIOR FILING DATE: 2000-08-09

PRIOR APPLICATION NUMBER: US 09/696,347

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 08/193,627

PRIOR FILING DATE: 1994-02-07

PRIOR APPLICATION NUMBER: US 07/882,712

PRIOR FILING DATE: 1992-05-14  
PRIOR APPLICATION NUMBER: US 09/436,430  
PRIOR FILING DATE: 1999-11-08  
NUMBER OF SEQ ID NOS: 6592

SOFTWARE: PatentIn version 3.2  
SEQ ID NO 3796  
LENGTH: 38

Qy 1 CCUGCAUCGAGUGAGCCGCUUAGGCCGAAAUU 34  
Db 1 CCUGCAACUGAGUGAGCCGCUUAGGCCGAAAUU 34

RESULT 10  
US-10-669-841-8687

Sequence 8687, Application US/10669841  
Publication No. US20040127446A1

GENERAL INFORMATION:

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Lawrence, Blact

APPLICANT: Dennis, Macejak

APPLICANT: James, McSwiggen

APPLICANT: David, Morrissey

APPLICANT: Pamela, Pavco

APPLICANT: Patrice, Lee

APPLICANT: Kenneth, Draper

APPLICANT: Elisabeth, Roberts

TITLE OF INVENTION: Oligonucleotide Mediated Inhibition of Hepatitis B Virus and HEPN

FILE REFERENCE: 400/04205 (MBH02-249-E)

CURRENT APPLICATION NUMBER: US/10/669,841

CURRENT FILING DATE: 2003-09-23

PRIOR APPLICATION NUMBER: PCT/US02/09187

PRIOR FILING DATE: 2002-03-26

PRIOR APPLICATION NUMBER: US 60/296,876

PRIOR FILING DATE: 2001-06-08

PRIOR APPLICATION NUMBER: US 60/335,059

PRIOR FILING DATE: 2001-10-24

PRIOR APPLICATION NUMBER: US 60/337,055

PRIOR FILING DATE: 2001-12-05

PRIOR APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: US 60/363,124

PRIOR FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 09/817,879

PRIOR FILING DATE: 2001-03-26

PRIOR APPLICATION NUMBER: US 09/740,332

PRIOR FILING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: US 09/611,931

PRIOR FILING DATE: 2000-07-07

PRIOR APPLICATION NUMBER: US 09/504,321

PRIOR FILING DATE: 2000-02-15

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 16207

SOFTWARE: PatentIn version 3.0

SEQ ID NO 8687

LENGTH: 38

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (31)..(33)  
OTHER INFORMATION: n stands for inosine  
US-10-669-841-8687

Query Match 82.6%; Score 31.4; DB 18; Length 38;  
Best Local Similarity 94.1%; Pred. No. 0.00053;  
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCUGCAUUCUGAUGAGCGCCGUAAGCCGAAAUUA 34  
DB 1 CCUGCAUUCUGAUGAGCGCCGUAAGCCGAAAUUA 34

RESULT 11  
US-10-138-674-11175  
Sequence 11175, Application US/10138674  
Publication No. US20040077565A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyne Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: MCSwigen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: MBH00-876-N (400/049)  
CURRENT APPLICATION NUMBER: US/10/138,674  
CURRENT FILING DATE: 2002-05-03  
NUMBER OF SEQ ID NOS: 20822  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 11175  
LENGTH: 38  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-138-674-11175

Query Match 82.1%; Score 31.2; DB 17; Length 38;  
Best Local Similarity 91.7%; Pred. No. 0.00065;  
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCUGCAUUCUGAUGAGCGCCGUAAGCCGAAAUUA 36  
DB 1 CCUGCAUUCUGAUGAGCGCCGUAAGCCGAAAUUA 36

RESULT 12  
US-10-138-674-11662  
Sequence 11662, Application US/10138674  
Publication No. US20040077565A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyne Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: MCSwigen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: MBH00-876-N (400/049)  
CURRENT APPLICATION NUMBER: US/10/138,674  
CURRENT FILING DATE: 2002-05-03  
NUMBER OF SEQ ID NOS: 20822  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 11662  
LENGTH: 38  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-10-138-674-11662

Query Match 82.1%; Score 31.2; DB 17; Length 38;  
Best Local Similarity 91.7%; Pred. No. 0.00065;  
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCUGCAUUCUGAUGAGCGCCGUAAGCCGAAAUUA 36  
DB 1 CCUGCAUUCUGAUGAGCGCCGUAAGCCGAAAUUA 36

RESULT 13  
US-10-287-949A-11175  
Sequence 11175, Application US/10287949A  
Publication No. US20040102389A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyne Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: MCSwigen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: MBH00-876-N (400/049)  
CURRENT APPLICATION NUMBER: US/10/287,949A  
CURRENT FILING DATE: 2003-04-11  
NUMBER OF SEQ ID NOS: 20822  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 11175  
LENGTH: 38  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-287-949A-11175

Query Match 82.1%; Score 31.2; DB 18; Length 38;  
Best Local Similarity 91.7%; Pred. No. 0.00065;  
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCUGCAUUCUGAUGAGCGCCGUAAGCCGAAAUUA 36  
DB 1 CCUGCAUUCUGAUGAGCGCCGUAAGCCGAAAUUA 36

RESULT 14  
US-10-287-949A-11662  
Sequence 11662, Application US/10287949A  
Publication No. US20040102389A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyne Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: MCSwigen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: MBH00-876-N (400/049)  
CURRENT APPLICATION NUMBER: US/10/287,949A  
CURRENT FILING DATE: 2003-04-11  
NUMBER OF SEQ ID NOS: 20822  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 11662  
LENGTH: 38  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-287-949A-11662

Query Match 82.1%; Score 31.2; DB 18; Length 38;  
Best Local Similarity 91.7%; Pred. No. 0.00065;  
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;



GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors  
FILE REFERENCE: MBH00-958-I (400/018)  
CURRENT APPLICATION NUMBER: US/09/848,754A  
CURRENT FILING DATE: 2001-05-03  
NUMBER OF SEQ ID NOS: 9645  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5340  
LENGTH: 38  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid  
NAME/KEY: misc feature  
LOCATION: (31)..(31)  
OTHER INFORMATION: n stands for inosine  
US-09-848-754A-5340

Query Match 80.5%; Score 30.6; DB 10; Length 38;  
Best Local Similarity 86.8%; Pred. No. 0.0012;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCUGCAUCUGAUGAGCGCCGUAGCGCGGAAAAAUCAG 38  
Db 1 CCUGCUGUCUGAUGAGCGCGUAGCGCGGAAAGAGG 38

RESULT 20  
US-10-156-306-1007  
Sequence 1007, Application US/10156306  
Publication No. US20030119017A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: McSwiggen, James  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
TITLE OF INVENTION: Levels of IKK-Gamma and PKR  
FILE REFERENCE: MBH01-664-A (400/050)  
CURRENT APPLICATION NUMBER: US/10/156,306  
CURRENT FILING DATE: 2002-05-28  
NUMBER OF SEQ ID NOS: 8013  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1007  
LENGTH: 38  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-156-306-1007

Query Match 80.5%; Score 30.6; DB 15; Length 38;  
Best Local Similarity 89.2%; Pred. No. 0.0012;  
Matches 33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCUGCAUCUGAUGAGCGCCGUAGCGCGGAAAAAUCAG 37  
Db 1 CUUGCGAUCUGAUGAGCGCGGUAGCGCGGAAAAAUCUG 37

RESULT 21  
US-10-138-674-11851  
Sequence 11851, Application US/10138674  
Publication No. US20040077565A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related  
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: MBH00-876-N (400/049)

CURRENT APPLICATION NUMBER: US/10/138,674  
CURRENT FILING DATE: 2002-05-03  
NUMBER OF SEQ ID NOS: 20822  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 11851  
LENGTH: 38  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-138-674-11851

Query Match 80.5%; Score 30.6; DB 17; Length 38;  
Best Local Similarity 89.2%; Pred. No. 0.0012;  
Matches 33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CUUGCAUCUGAUGAGCGCCGUAGCGCGGAAAAAUCAG 38  
Db 2 CUUGCAUCUGAUGAGCGCCGUAGCGCGGAAAAAUCAG 38

RESULT 22  
US-10-287-949A-11851  
Sequence 11851, Application US/10287949A  
Publication No. US20040102389A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related  
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: MBH00-876-N (400/049)  
CURRENT APPLICATION NUMBER: US/10/287,949A  
CURRENT FILING DATE: 2003-04-11  
NUMBER OF SEQ ID NOS: 20822  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 11851  
LENGTH: 38  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-287-949A-11851

Query Match 80.5%; Score 30.6; DB 18; Length 38;  
Best Local Similarity 89.2%; Pred. No. 0.0012;  
Matches 33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CUUGCAUCUGAUGAGCGCCGUAGCGCGGAAAAAUCAG 38  
Db 2 CUUGCAUCUGAUGAGCGCCGUAGCGCGGAAAAAUCAG 38

RESULT 23  
US-09-780-533A-3295  
Sequence 3295, Application US/09780533A  
Publication No. US20030060611A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Blact, Larry  
APPLICANT: McSwiggen, Jim  
APPLICANT: Chowhira, Bharat  
APPLICANT: Haebertl, Pete  
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
FILE REFERENCE: MBH00,878-A (400/011)  
CURRENT APPLICATION NUMBER: US/09/780,533A  
CURRENT FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: US 60/181,797  
PRIOR FILING DATE: 2000-02-11  
NUMBER OF SEQ ID NOS: 6679  
SOFTWARE: PatentIn version 3.0

```

; SEQ ID NO 3295
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-533A-3295

Query Match
Best Local Similarity 80.0%; Score 30.4; DB 10; Length 38;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db
5 CAUCUGAUGAGCGCCGUAUAGCGCGAANAUA 36
5 CAACUGAUGAGCGCCGUAUAGCGCGAANAUA 36

RESULT 24
US-09-780-533A-3992
; Sequence 3992, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrita, Bharat
; APPLICANT: Haeblerl, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00, 878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3992
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-780-533A-3992

Query Match
Best Local Similarity 80.0%; Score 30.4; DB 10; Length 38;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db
2 CUGCAUUCUGAUGAGCGCCGUAUAGCGCGAANAUA 34
2 CUGCAUUCUGAUGAGCGCCGUAUAGCGCGAANAUA 34

RESULT 25
US-09-848-754A-4314
; Sequence 4314, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4314
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```

; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
US-09-848-754A-4314

Query Match
Best Local Similarity 80.0%; Score 30.4; DB 10; Length 38;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db
7 AUCUGAUGAGCGCCGUAUAGCGCGAANAUCAG 38
7 AUCUGAUGAGCGCCGUAUAGCGCGAANAUCAG 38

RESULT 26
US-09-780-164-1164
; Sequence 1164, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1164
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-164-1164

Query Match
Best Local Similarity 80.0%; Score 30.4; DB 10; Length 38;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db
5 CAUCUGAUGAGCGCCGUAUAGCGCGAANAUA 36
5 CAUCUGAUGAGCGCCGUAUAGCGCGAANAUA 36

RESULT 27
US-10-138-674-11690
; Sequence 11690, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11690
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-11690

Query Match
Best Local Similarity 80.0%; Score 30.4; DB 17; Length 38;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 CCUGCAUUCUGAGCGCCGUUAGCCGAAAA 32  
DB 1 CCUGCAAGCUGAGCGCCGUUAGCGCGAAAA 32

RESULT 28  
US-10-138-674-12840  
; Sequence 12840, Application US/10138674  
; Publication No. US20040077565A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: MCSwigen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12840  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-138-674-12840

Query Match 80.0%; Score 30.4; DB 17; Length 38;  
Best Local Similarity 96.9%; Pred. No. 0.0015;  
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 AUCUGAUGAGCGCCGUUAGCGCGAAAAAUCAGG 38  
DB 7 AGCUGAUGAGCGCCGUUAGCGCGAAAAAUCAGG 38

RESULT 29  
US-10-287-949A-11690  
; Sequence 11690, Application US/10287949A  
; Publication No. US20040102389A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: MCSwigen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/287,949A  
; CURRENT FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 11690  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-287-949A-11690

Query Match 80.0%; Score 30.4; DB 18; Length 38;  
Best Local Similarity 96.9%; Pred. No. 0.0015;  
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCUGCAUUCUGAGCGCCGUUAGCGCGAAAA 32  
DB 1 CCUGCAAGCUGAGCGCCGUUAGCGCGAAAA 32

RESULT 30  
US-10-287-949A-12840  
; Sequence 12840, Application US/10287949A  
; Publication No. US20040102389A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: MCSwigen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/287,949A  
; CURRENT FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12840  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-287-949A-12840

US-10-287-949A-12840

Query Match 80.0%; Score 30.4; DB 18; Length 38;  
Best Local Similarity 96.9%; Pred. No. 0.0015;  
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 AUCUGAUGAGCGCCGUUAGCGCGAAAAAUCAGG 38  
DB 7 AGCUGAUGAGCGCCGUUAGCGCGAAAAAUCAGG 38

RESULT 31  
US-09-780-533A-3424  
; Sequence 3424, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: MCSwigen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haebel, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MHB00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3424  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-780-533A-3424

Query Match 79.5%; Score 30.2; DB 10; Length 38;  
Best Local Similarity 91.4%; Pred. No. 0.0018;  
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCUGCAUUCUGAGCGCCGUUAGCGCGAAAAUCA 36  
DB 2 CUGCAACCTUGAGAGCGCCGUUAGCGCGAAAACTAA 36

RESULT 32  
US-10-138-674-10420  
; Sequence 10420, Application US/10138674

Publication No. US20040077565A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
FILE REFERENCE: MBH00-876-N (400/049)  
CURRENT APPLICATION NUMBER: US/10/138,674  
NUMBER OF SEQ ID NOS: 20822  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 10420  
LENGTH: 38  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-138-674-10420

Query Match  
Best Local Similarity 79.5%; Score 30.2; DB 17; Length 38;  
Best Local Similarity 91.4%; Pred. No. 0.0018; 3; Indels 0; Gaps 0;  
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CUGCAUUCUGAUGAGCCGCUUAGCCGGAUUA 36  
DB 2 CUACAGUCUGAUGAGCCGCUUAGCCGGAUUA 36

RESULT 33  
US-10-287-949A-10420  
Sequence 10420, Application US/10287949A  
Publication No. US20040102389A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
FILE REFERENCE: MBH00-876-N (400/049)  
CURRENT APPLICATION NUMBER: US/10/287,949A  
NUMBER OF SEQ ID NOS: 20822  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 10420  
LENGTH: 38  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-287-949A-10420

Query Match  
Best Local Similarity 79.5%; Score 30.2; DB 18; Length 38;  
Best Local Similarity 91.4%; Pred. No. 0.0018; 3; Indels 0; Gaps 0;  
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CUGCAUUCUGAUGAGCCGCUUAGCCGGAUUA 36  
DB 2 CUACAGUCUGAUGAGCCGCUUAGCCGGAUUA 36

RESULT 34  
US-09-927-046-2660  
Sequence 2660, Application US/09927046  
Publication No. US20030064946A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc  
APPLICANT: McSwiggen, Jim  
APPLICANT: Thompson, Jim

APPLICANT: McKenzie, Tim  
APPLICANT: Ayers, Dave  
APPLICANT: Grupe, Andrew  
APPLICANT: Szymkowski, Edmund  
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric  
FILE REFERENCE: 249/021  
CURRENT APPLICATION NUMBER: US/09/927,046  
CURRENT FILING DATE: 2001-08-09  
NUMBER OF SEQ ID NOS: 5450  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2660  
LENGTH: 38  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-927-046-2660

Query Match  
Best Local Similarity 78.9%; Score 30; DB 10; Length 38;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCAUUCUGAUGAGCCGCUUAGCCGGAUUA 33  
DB 4 GCAUUCUGAUGAGCCGCUUAGCCGGAUUA 33

RESULT 35  
US-09-877-478-2631  
Sequence 2631, Application US/09877478  
Publication No. US20030068301A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Draper, Kenneth  
APPLICANT: Blatt, Larry  
APPLICANT: McSwiggen, Jim  
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication  
FILE REFERENCE: MBH00-845-H (400/029)  
CURRENT APPLICATION NUMBER: US/09/877,478  
CURRENT FILING DATE: 2001-12-31  
PRIOR APPLICATION NUMBER: US 07/882,712  
PRIOR FILING DATE: 1992-05-14  
PRIOR APPLICATION NUMBER: US 09/531,025  
PRIOR FILING DATE: 2000-03-20  
PRIOR APPLICATION NUMBER: US 09/636,385  
PRIOR FILING DATE: 2000-08-09  
PRIOR APPLICATION NUMBER: US 09/696,347  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 08/193,627  
PRIOR FILING DATE: 1994-02-07  
PRIOR APPLICATION NUMBER: US 08/433,993  
PRIOR FILING DATE: 1995-05-04  
PRIOR APPLICATION NUMBER: US 08/434,504  
PRIOR FILING DATE: 1995-05-04  
PRIOR APPLICATION NUMBER: US 09/436,430  
PRIOR FILING DATE: 1999-11-08  
NUMBER OF SEQ ID NOS: 6586  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2631  
LENGTH: 38  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-877-478-2631

Query Match  
Best Local Similarity 78.9%; Score 30; DB 10; Length 38;  
Best Local Similarity 86.8%; Pred. No. 0.0022;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCUGCAUUCUGAUGAGCCGCUUAGCCGGAUUA 38

Db 1 CCACAGCUGAUGAGCCCGUAGCCGGAAGAUAGG 38

RESULT 36

US-09-848-754A-4081

Sequence 4081, Application US/09848754A

Publication No. US20030073207A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related

TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors

FILE REFERENCE: MBH00-958-I (400/018)

CURRENT APPLICATION NUMBER: US/09/848,754A

CURRENT FILING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 9645

SOFTWARE: Patent version 3.0

SEQ ID NO 4081

LENGTH: 38

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid

US-09-848-754A-4081

Query Match

Best Local Similarity 78.9%; Score 30; DB 10; Length 38;

Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCUGCAUCUGAUGAGCCCGUAGCCGGAAGAUAGG 38

Db 1 CCUGCAUCUGAUGAGCCCGUAGCCGGAAGAUAGG 38

RESULT 37

US-09-776-474-1268

Sequence 1268, Application US/09776474

Publication No. US20030087847A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Jarvis, Thale

APPLICANT: Bochner, Robert

APPLICANT: Holman, Patricia

APPLICANT: Fattaey, Ali

APPLICANT: McSwigen, Jim

TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK

TITLE OF INVENTION: Enzyme

FILE REFERENCE: MBH00-955-A (400/008)

CURRENT APPLICATION NUMBER: US/09/776,474

CURRENT FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: US 60/179,983

PRIOR FILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 2992

SOFTWARE: Patent version 3.0

SEQ ID NO 1268

LENGTH: 38

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

US-09-776-474-1268

Query Match

Best Local Similarity 78.9%; Score 30; DB 10; Length 38;

Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCUGCAUCUGAUGAGCCCGUAGCCGGAAGAUAGG 38

Db 1 CCUGCAUCUGAUGAGCCCGUAGCCGGAAGAUAGG 38

RESULT 38

US-10-156-306-814

Sequence 814, Application US/10156306

Publication No. US20030119017A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwigen, James

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related

TITLE OF INVENTION: Levels of IKK-gamma and PKR

FILE REFERENCE: MBH01-664-A (400/050)

CURRENT APPLICATION NUMBER: US/10/156,306

CURRENT FILING DATE: 2002-05-28

NUMBER OF SEQ ID NOS: 8013

SOFTWARE: Patent version 3.0

SEQ ID NO 814

LENGTH: 38

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-10-156-306-814

Query Match

Best Local Similarity 78.9%; Score 30; DB 15; Length 38;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AUCUGAUGAGCCCGUAGCCGGAAGAUAGG 35

Db 6 AUCUGAUGAGCCCGUAGCCGGAAGAUAGG 35

RESULT 39

US-10-156-306-4583

Sequence 4583, Application US/10156306

Publication No. US20030119017A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwigen, James

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related

TITLE OF INVENTION: Levels of IKK-gamma and PKR

FILE REFERENCE: MBH01-664-A (400/050)

CURRENT APPLICATION NUMBER: US/10/156,306

CURRENT FILING DATE: 2002-05-28

NUMBER OF SEQ ID NOS: 8013

SOFTWARE: Patent version 3.0

SEQ ID NO 4583

LENGTH: 38

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-10-156-306-4583

Query Match

Best Local Similarity 78.9%; Score 30; DB 15; Length 38;

Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCUGCAUCUGAUGAGCCCGUAGCCGGAAGAUAGG 38

Db 1 CCUGCAUCUGAUGAGCCCGUAGCCGGAAGAUAGG 38

RESULT 40

US-10-342-902-2631

Sequence 2631, Application US/10342902

Publication No. US20040054156A1

GENERAL INFORMATION:

APPLICANT: Sina Therapeutics, Inc.

APPLICANT: Draper, Kenneth

APPLICANT: Blact, Larry

APPLICANT: McSwigen, Jim

APPLICANT: Morrissey, Dave

TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication

FILE REFERENCE: 400/075 (MBH00-845-I)

CURRENT APPLICATION NUMBER: US/10/342,902

```

; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 2631
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
us-10-342-902-2631

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Query Match      78.9%; Score 30; DB 17; Length 38;
Best Local Similarity 86.8%; Pred. No. 0.0022;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY      1 CCUGCAUUCGUAUGAGCGCGUUGAGCGCGAAGAAUUCAGG 38
DB      1 CCACAGAGCUGAUGAGCGCGUUGAGCGCGAAGAAUUCAGG 38

```

Search completed: May 13, 2005, 18:25:02  
Job time : 326.036 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2005, 16:42:23 ; Search time 1848.87 Seconds  
(without alignments)  
782.337 Million cell updates/sec

Title: US-09-927-046-2332

Perfect score: 38  
Sequence: 1 ccgcaucugaugagcgccguuagggcgcaaaaucag 38

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 675282

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :  
EST:  
1: gb\_ecl1:\*  
2: gb\_ecl2:\*  
3: gb\_hic:\*  
4: gb\_esc3:\*  
5: gb\_esc4:\*  
6: gb\_esc5:\*  
7: gb\_esc6:\*  
8: gb\_gsa1:\*  
9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	17.6	46.3	63 1	AI313954 u149601.Y
2	17.2	45.3	59 8	AZ368574 1M0118A16
3	17	44.7	70 1	AA666597 vm49401.r
4	17	44.7	84 9	AL765388 Arabidops
5	17	44.7	92 8	BH803188 1008099D0
6	17	44.7	94 8	AZ807494 2M0070F19
7	16.8	44.2	50 1	AU105965 AU105965
8	16.8	44.2	50 1	AU105967 AU105967
9	16.8	44.2	55 1	AI341480 qg94b11.x
10	16.6	43.7	91 1	AV536751 AV536751
11	16.4	43.2	67 9	BX655236 Arabidops
12	16.4	43.2	100 7	CN165896 996741.MA
13	16.2	42.6	90 8	BH913847 3526.1.41
14	16.2	42.6	73 6	CD971713 OME17h01
15	16	42.1	82 9	AJ597197 Arabidops
16	16	42.1	91 4	BU029544 BU029544
17	16	42.1	94 1	AI204769 ZF-EST88
18	16	42.1	97 1	AA237314 mx17b12.r
19	15.8	41.6	65 8	AZ391476 1M0153C11
20	15.8	41.6	69 6	CA567380 LHE11p67P
21	15.8	41.6	72 6	CD963815 SPY_106
22	15.8	41.6	76 6	CA796314 CAG_BL_33
23	15.8	41.6	89 4	BG062646 L0955G10-
24	15.8	41.6	92 9	CG663893 OST450022

C 25	15.8	41.6	94 6	CD947628 SAA_70 Ge
C 26	15.8	41.6	94 7	CV519527
C 27	15.8	41.6	94 9	CG528153 OST1071142
C 28	15.8	41.6	97 8	AZ608536 1M0432N13
C 29	15.8	41.6	98 8	AZ481971
C 30	15.8	41.6	98 8	AZ566002 215PVB01
C 31	15.6	41.1	41 9	AJ590916 Arabidops
C 32	15.6	41.1	76 1	AI702572 w68D03.x
C 33	15.6	41.1	76 7	w72704
C 34	15.6	41.1	78 9	CG547582 OST148394
C 35	15.6	41.1	80 9	CG545569 OST143941
C 36	15.6	41.1	90 1	AA286563 v084e07.r
C 37	15.6	41.1	97 1	AI1318202 ta52a03.x
C 38	15.6	41.1	99 4	BG881971 eae92c02.
C 39	15.6	41.1	100 7	CV316867 CM2-BM018
C 40	15.4	40.5	51 9	CC483070 CH240.311
C 41	15.4	40.5	56 9	BX286908 Arabidops
C 42	15.4	40.5	77 6	CD531375 10110 Ara
C 43	15.4	40.5	79 1	AA889445 AJ81h12.8
C 44	15.4	40.5	80 8	AZ502082 1M0341N09
C 45	15.4	40.5	82 4	BG673231 DRNBOD07
C 46	15.4	40.5	84 1	AL666581 AL666581
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C 49	15.4	40.5	88 1	AA474045 v654D03.r
C 50	15.4	40.5	92 5	BU655365 1112119E0
C 51	15.4	40.5	100 7	CF917848 HD-07-L0
C 52	15.4	40.5	100 9	BX002767 Arabidops
C 53	15.2	40.0	48 8	AZ331129 1M0056M21
C 54	15.2	40.0	50 1	AU105968 AU105968
C 55	15.2	40.0	61 1	AI1318033 ta75g02.x
C 56	15.2	40.0	66 3	AY432564 Aedes aeg
C 57	15.2	40.0	76 8	BH011379 BG01292-5
C 58	15.2	40.0	79 8	AZ918914 1006013C0
C 59	15.2	40.0	81 8	AZ920216 1006018G0
C 60	15.2	40.0	82 1	AI1973602 ec07B01.Y
C 61	15.2	40.0	84 8	AZ587706 1M0359L01
C 62	15.2	40.0	84 8	AZ918688 1006005F0
C 63	15.2	40.0	86 8	AZ918789 1006007G1
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C 65	15.2	40.0	92 8	BZ424945 100022272
C 66	15.2	40.0	92 9	AL952395 Arabidops
C 67	15.2	40.0	92 9	CG734095 1119162G0
C 68	15.2	40.0	95 9	CG617247 OST110506
C 69	15.2	40.0	96 1	AJ742933 AJ742933
C 70	15.2	40.0	99 2	BE613971 601504092
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C 73	15	39.5	76 7	CN850154 000917A9F
C 74	15	39.5	77 9	CG510398 OST62098
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C 76	15	39.5	81 1	AV858416 AV858416
C 77	15	39.5	88 4	BM114142 ACS62-DMS
C 78	15	39.5	89 9	CG537563 OST12682
C 79	15	39.5	95 9	AJ587756 Arabidops
C 80	15	39.5	96 2	BF137294 601781654
C 81	15	39.5	100 4	BJ263250 BJ263250
C 82	14.8	38.9	50 9	BX977848 Forward.8
C 83	14.8	38.9	52 2	AM696628 NF107B115
C 84	14.8	38.9	57 2	AM633542 b109607.w
C 85	14.8	38.9	57 8	B02241 CSR1-150B11
C 86	14.8	38.9	63 6	CB070218 1627612.Y
C 87	14.8	38.9	63 9	CG653178 OST146535
C 88	14.8	38.9	68 9	CG546732 OST146535
C 89	14.8	38.9	73 4	BI094826 EST-CD34N
C 90	14.8	38.9	75 9	CG512276 OST65121
C 91	14.8	38.9	77 6	CD944539 RDX_19 Ge
C 92	14.8	38.9	77 6	CD965817 SEL_217 G
C 93	14.8	38.9	79 1	AA929672 vY75B09.r
C 94	14.8	38.9	80 9	CG558020 OST433475
C 95	14.8	38.9	83 9	CR137364 Reverse.8
C 96	14.8	38.9	87 1	AJ540137
C 97	14.8	38.9	87 4	BI546018 603188148

C 98 14.8 38.9 87 8 BH609273 2896 L1.8  
 C 100 14.8 38.9 91 8 BH903262 1023  
 C 100 14.8 38.9 92 6 CB395266 15264

ALIGNMENTS

RESULT 1  
 LOCUS A133954  
 DEFINITION A133954 63 bp mRNA linear EST 17-DEC-1998  
 u149c01.y1 Sugano mouse liver mlia mus musculus cDNA clone  
 IMAGE:1923264.5 similar to gb:U03524 Mouse mRNA for group 1 major  
 urinary protein (MOUSE);, mRNA sequence.

ACCESSION A133954.1 GI:4029080  
 VERSION A133954  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 63)  
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
 Waterston,R.  
 TITLE The WashU-HMI Mouse EST Project  
 JOURNAL Unpublished (1996)  
 COMMENT Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu

FEATURES  
 source This clone is available royalty-free through LML; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:979556  
 Tracer considered overall poor quality  
 Seq primer: custom primer used  
 High quality sequence stop: 1.  
 location/Qualifiers  
 1..63

/organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL"  
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 /clone="IMAGE:1923264"  
 /sex="female"  
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 /lab\_host="DHL0B"  
 /clone\_lib="Sugano mouse liver mlia"  
 /note="Organ: liver; Vector: pME18-F13; Site\_1: DraIII  
 (CACGCTGTG); Site\_2: DraIII (CACGCTGTG); 1st strand cDNA  
 was primed with an oligo(dT) primer  
 [ATGGGCGCTTTTCTTTTCTTTT]; double-stranded cDNA was  
 ligated to a DraIII adaptor (TTTGGCTACTGG), digested  
 and cloned into distinct DraIII sites of the pME18-F13  
 vector (5' site CACGCTGTG, 3' site CACGCTGTG). XhoI should  
 be used to isolate the cDNA insert. Size selection was  
 performed to exclude fragments <1.5kb. Library  
 constructed by Dr. Sumio Sugano (University of Tokyo  
 Institute of Medical Science). Custom primers for  
 sequencing: 5' end primer CTTGCGCTCTAAGCTGCG and 3' end  
 primer CGACTGCACTCGACGACACA."

ORIGIN

Query Match 46.3%; Score 17.6; DB 1; Length 63;  
 Best Local Similarity 59.4%; Pred. No. 7.9e+03;  
 Matches 19; Conservative 4; Mismatches 9; Indels 0; Gaps 0;  
 1 CTUGCAUUCUGAUGAGCCGUGAGCCGAGAAA 32

Db 11  
 CCTTCAGCTGATGGGTGTGTATGCGCCGAGAA 42

RESULT 2  
 LOCUS A2368574 59 bp DNA linear GSS 02-OCT-2000  
 DEFINITION 1M0118A16R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
 clone UGCGIM0118A16 R, genomic survey sequence.  
 ACCESSION A2368574  
 VERSION A2368574.1 GI:10482274  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 59)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112 USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0118 row: A column: 16  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 59.  
 location/Qualifiers  
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/organism="Mus musculus"  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCGIM0118A16"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCGIM library"  
 /note="Vector: pMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD2 (gi14732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

ORIGIN

Query Match 45.3%; Score 17.2; DB 8; Length 59;  
 Best Local Similarity 53.3%; Pred. No. 1.2e+04;  
 Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
 8 UCUGAUGAGCCGUGAGCCGAGAAAUCAG 37

**RESULT 3**

Locus Definition	Accession Version Keywords	Organism Source	Reference Authors	Title Journal Comment	Features Source
Aa66597/c LOCUS DEFINITION  AL765388/C AL765388 VERSION KEYWORDS	AA66597 U99d01.r1 Scratogene mouse Tcell 93731 Mus musculus cDNA clone IMAGE1001569 s. similar to SW:RJ34_HUMAN P49207 60S RIBOSOMAL PROTEIN L34 . ; mRNA sequence. AA66597 AA66597.1 GI:2625298 EST.	Mus musculus (house mouse) Mus musculus Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumetaria; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 70)	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubnue,T... Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,U., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Thelsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.	The WashU-HMI Mouse EST Project Unpublished (1996) Contact: Marra M/Mouse EST project WashU-HMI Mouse EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: mousesest@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMGC Consortium ( <a href="#">info@image.llnl.gov</a> ) for further information. GSI:565785	/organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="IMAGE:1001569" /tissue.type="Tcell" /dev_stage="M30 CD4+ cells" /lab_host="SOJR (kanamycin resistant)" /clone_1lb="Scratogene mouse Tcell 93731" /note="Organ: blood; Vector: pbluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb; Uni-ZAP XR Vector.; -5' adaptor sequence: 5' GAATCGCACACAGC 3'-3' adaptor sequence: 5' CTCGACTTTTTTTTTTTTTT 3'"

SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE	1. Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weisshaar, B. GABI-Kat Simplesearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana Bioinformatics 19 (11), 1441-1442 (2003)
JOURNAL	Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE	22755829
PUBMED	12874060
REFERENCE	2. Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B. An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
JOURNAL	Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE	23117147
PUBMED	14756321
REFERENCE	3. Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weisshaar, B. High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines Biotechniques 35 (6), 1164-1168 (2003)
JOURNAL	Biotechniques 35 (6), 1164-1168 (2003)
MEDLINE	14682050
PUBMED	4 (bases 1 to 84) Rosso, M.G., Strizhov, N., Li, Y. and Weisshaar, B. Direct Submission Submitted (31-MAR-2004) weisshaar.B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone F2J3. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpibz-koeln.mpg.de/GABI-Kat/ Location/Qualifiers
JOURNAL	Location/Qualifiers
MEDLINE	1. .84 /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /strain="Columbia 0" /db_xref="taxon:3702" /clone="GK-138F10-012752" /clone_1fb="Arabidopsis thaliana T-DNA insertion lines" /ecotype="Col-0" /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pACT161 (GenBank accession number: A2537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
JOURNAL	Query Match 44.7%; Score 17; DB 9; Length 84;
MEDLINE	Best Local Similarity 55.9%; Pred. No. 1.5e+04;
PUBMED	Matches 19; Conservative 4; Mismatched 11; Indels 0; Gaps 0;
REFERENCE	2 CUGCAUCUGAGGCCGCUUAGCCGGAATAAUC 35      :       :     :     : 44 CAGCAATCTGTAAAGGCNTTCAGTTCCGGAAATC 11
JOURNAL	DB 92 bp DNA linear GSS 25-APR-2002
MEDLINE	BH803188
PUBMED	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
JOURNAL	Survey Project
MEDLINE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
PUBMED	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
REFERENCE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
JOURNAL	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
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JOURNAL	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
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REFERENCE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
JOURNAL	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
MEDLINE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
PUBMED	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
REFERENCE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
JOURNAL	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
MEDLINE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
PUBMED	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
REFERENCE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
JOURNAL	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
MEDLINE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
PUBMED	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
REFERENCE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
JOURNAL	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
MEDLINE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
PUBMED	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
REFERENCE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
JOURNAL	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
MEDLINE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
PUBMED	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
REFERENCE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
JOURNAL	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
MEDLINE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
PUBMED	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
REFERENCE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
JOURNAL	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
MEDLINE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
PUBMED	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
REFERENCE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
JOURNAL	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
MEDLINE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
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REFERENCE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
JOURNAL	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
MEDLINE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
PUBMED	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
REFERENCE	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
JOURNAL	1008099D07.2HL.y2 1008 - RescueMu GfId I Zea mays genomic, genomic survey project.
MEDLINE	100





Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 91)

Asanizu, E., Nakamura, Y., Sato, S. and Tabata, S.

A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries

DNA Res. 7 (3), 175-180 (2000)

20363093

10907847

CONTACT: Erika Asanizu

The First Laboratory for Plant Gene Research

Kazusa DNA Research Institute

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan

Email: asanizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.

Location/Qualifiers

1..91

/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/ecotype="Columbia"

/db\_xref="taxon:3702"

/clone="PAZNI10502R"

/tissue\_type="liquid-cultured seedlings"

/clone\_lib="Arabidopsis thaliana liquid-cultured seedlings Columbia"

/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2: XhoI"

ORIGIN

Query Match 43.7%; Score 16.6; DB 1; Length 91;

Best Local Similarity 51.6%; Pred. No. 2.3e+04;

Matches 16; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

3 UGCAUUCGAGUAGCGCGUAGCGCAAA 33

91 TGCATTTGTTCCAAAGGTTAAGTGAAAA 61

RESULT 11

LOCUS BX655236 67 bp DNA linear GSS 04-APR-2004

DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-587H12-021350, genomic survey sequence.

ACCESSION BX655236

VERSION BX655236.1 GI:37611624

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1

Li, Y., Rosso, M.G., Strizhov, N., Viehovever, P. and Weisshaar, B.

GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana

Bioinformatics 19 (11), 1441-1442 (2003)

22755829

12874060

2

Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.

An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics

Plant Mol. Biol. 53 (1-2), 247-259 (2003)

23117147

14756321

3

Strizhov, N., Li, Y., Rosso, M.G., Viehovever, P., Dekker, K.A. and Weisshaar, B.

High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

Biotechniques 35 (6), 1164-1168 (2003)

14682050

4 (bases 1 to 67)

Li, Y., Strizhov, N., Rosso, M.G. and Weisshaar, B.

Direct Submission

Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At1g55130.

Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

Location/Qualifiers

1..67

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="GK-587H12-021350"

/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pGAB1 (Genbank accession number: AY529716). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 43.2%; Score 16.4; DB 9; Length 67;

Best Local Similarity 58.8%; Pred. No. 2.7e+04;

Matches 20; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

4 GCAUUCGAGUAGCGCGUAGCGCAAAUACG 37

14 GAAACGATGTAGCGCGTTAGCAGCAAAACGAG 47

RESULT 12

LOCUS CN165896/c 100 bp mRNA linear EST 02-APR-2004

DEFINITION 996741 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence.

ACCESSION CN165896

VERSION CN165896.1 GI:46180326

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 100)

Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonnenman, D.J., Wray, J.E. and Keeler, J.W.

Porcine EST collection using a normalized library constructed from embryos representing early developmental stages

Unpublished (2003)

CONTACT: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim\_alt option. Vector identified with cross\_match v0.990329.

Plate: TMM8065 row: B column: 17

Seq primer: TAGAAGACAGTCGAGG.

Location/Qualifiers

1..100

/organism="Sus scrofa"

```

/mol_type="mRNA"
/db_xref="taxon:9823"
/ligase_type="pooled"
/lab_host="DH10B"
/clone_lig="MARC 4PIG"
notes="Vector: pCDNA3.1, Site 1: EcoRI, Site 2: NotI
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
ORIGIN

```

QY	5	CAATCTGATAGGCGCCGUAAGCCGCAAAAATATAGG	38
		: : :       : :	
Db	84	CAAAATCTCTAGGCACTGTAGGCAAGACAGAAAGC	51

Query Match 43.2%, Score 16.4; DB 7 Length 100;  
 Best Local Similarity 58.8%, Pred. No.2.8e+04;  
 Matches 20; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

RESULT 13	LOCUS	DEFINITION	ACCSSION	VERSION	KEYWORDS	SOURCE	ORGANISM
BH913847	BH913847	356-141_1_C09_2EL_x_1 3526 - Rescuetm Grid K Zea mays genomic.	BH913847	BH913847	GSS.	Zea mays	Zea mays

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	(bases 1 to 90)	Walbot, V.	Maize genomic sequences found using engineered RescuerMu transposon	
		Unpublished (2001)		
		Contact: Walbot V		
		Department of Biological Sciences		
		Stanford University		
		855 California Ave, Palo Alto, CA 94304, USA		
		Tel: 650 723 3227		
		Fax: 650 725 8221		
		Email: walbot@stanford.edu		
		Possible ligation site of ends cut by 2 different endonucleases.		
		Reverse complemented post-ligation sequence from source sequence.		
		Plasm: 3526.1.41.1 row: 8		
		Class: transposon-tagged		
		Location/Qualifiers		
		1..90		

ORIGIN	
Query Match	42.6%; Score 16.2; DB 8; Length 90;
Beet Local Similarity	62.1%; Pred. No. 3.4e+04;

	Matches	18;	Conservative	3;	Mismatches	8;	Indels	0;	Gaps	0;
QY		1	CCUCGAUCGAGGAGGCCGUAAGCCGA	29						
			: : : : : : : :							
Db		45	CCTGGAGACTGAAGAGACGCTCGCCAA	73						

RESULT 14	
CD971713	
LOCUS	
DEFINITION	OAE12h01.yg QAE zea mays 73 bp mRNA linear EST 16-JUL-2003
ACCESSION	CD971713
VERSION	CD971713.1 GI:32832035
KEYWORDS	EST.
SOURCE	Zea mays
ORGANISM	Zea mays

**FEATURES**  
**SOURCE**

## ORIGIN

Query Match	42.1%	Score 16	DB 6	Length 73
Best Local Similarity	62.5%	Prod. No.	4.1e+04	
Matches	20	Conservative	2	Mismatches 10
				Indels 0
				Gaps 0

RESULT 15	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AJ597197	82 bp DNA	linear	GSS 15-JAN-2000				
		Arabidopsis thaliana T-DNA flanking sequence, left border, clone 447A09, genomic survey sequence.	AJ597197				
			AJ597197				
			AJ597197.1	GI:37946825			
					GSS; left border; T-DNA flanking sequence.		
					Arabidopsis thaliana (thale cress)		
					Arabidopsis thaliana		

REFERENCE	1
AUTHORS	Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chavain, S., Bechold, N., Cruaud, C., Derose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.
TITLE	T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL	EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE	22363535
PUBMED	12446565

REFERENCE 2 (bases 1 to 82)  
AUTHORS Balzerque, S.  
TITLE Direct Submission  
JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue  
Gaston Cremieux, 91057 Evry cedex, FRANCE

COMMENT PCR was performed on DNA from transformants of *Arabidopsis thaliana* plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).  
Location/Qualifiers

FEATURES  
source 1..82  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Massillawskija"  
/db\_xref="taxon:3702"  
/clone="447A09"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
misc\_feature 1..82  
/note="T-DNA flanking sequence  
left border"

ORIGIN  
Query Match 42.1%; Score 16; DB 9; Length 82;  
Best Local Similarity 57.6%; Pred. No. 4.1e+04;  
Matches 19; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 6 AAUCGAGAGCGCCGUAAGCCGAAAUACAG 38  
||:|||||  
1 AATATGATTAGCCCTCAGGACNAAAAAACAG 33

Db 1

RESULT 16  
BU029544 91 bp mRNA linear EST 26-SEP-2003  
LOCUS BU029544 NIBB Mochii normalized Xenopus neurola library Xenopus  
DEFINITION laevis cDNA clone X1012m10 5', mRNA sequence.  
ACCESSION BU029544  
VERSION BU029544.1 GI:17369178  
KEYWORDS EST.  
SOURCE Xenopus laevis (African clawed frog)  
ORGANISM Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
Xenopodinae; Xenopus; Xenopus.  
1 (bases 1 to 91)  
Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-I, T. and Kohara, Y.  
Expressed genes in *X. laevis* embryo  
Unpublished (2001)  
Contact: Tadao Shin-I  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: [tshini@genes.nig.ac.jp](mailto:tshini@genes.nig.ac.jp)  
The information of this clone is available through the following URL.  
<http://xenopus.nibb.ac.jp>.  
Location/Qualifiers  
1..91  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="X1012m10"  
/tissue\_type="whole embryo"

FEATURES  
source

ORIGIN  
Query Match 42.1%; Score 16; DB 4; Length 91;  
Best Local Similarity 70.8%; Pred. No. 4.2e+04;  
Matches 17; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 8 UCUGAGAGCGCCGUAAGCCGAA 31  
:|||||  
15 TCTGAAGAGCCGACAGCTGAA 38

Db 15

RESULT 17  
AI204769 94 bp mRNA linear EST 14-OCT-1998  
LOCUS ZF-EST88 zebrafish cDNA library Danio rerio cDNA clone M88 3',  
DEFINITION mRNA sequence.  
ACCESSION AI204769  
VERSION AI204769.1 GI:3757375  
KEYWORDS EST.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 94)  
Huh, T.L., Park, H.C., Yeo, S.Y., Hong, S.K. and Kim, S.H.  
Rapid identification and isolation of zebrafish cDNA clones  
(Huh, T.L. et al.)  
Unpublished (1998)  
Contact: Tae-Il, Huh  
Department of Genetic Engineering  
College of Natural Sciences, Kyungpook National University  
1370 Bankyuk-dong, Pukku, Taegu 702-701, S. Korea  
Tel: +82 53 950 5387  
Fax: +82 53 943 9755  
Email: [tlhuh@kyungpook.ac.kr](mailto:tlhuh@kyungpook.ac.kr)  
Insert Length: 94 Std Error: 0.00  
Seq primer: T7 promoter primer  
High quality sequence stop: 93.  
Location/Qualifiers  
1..94  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="M88"  
/sex="male and female mix"  
/tissue\_type="embryonic"  
/dev\_stage="6 - 48 hours post fertilization"  
/clone\_lib="Zebrafish cDNA library"

FEATURES  
source

ORIGIN  
Query Match 42.1%; Score 16; DB 1; Length 94;  
Best Local Similarity 53.1%; Pred. No. 4.2e+04;  
Matches 17; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 6 AAUCGAGAGCGCCGUAAGCCGAAAUACAG 37  
||:|||||  
34 AATCGATGATGTCTTCGACAGATCTCG 65

Db 34

RESULT 18  
AA237314 97 bp mRNA linear EST 03-MAR-1997  
LOCUS AA237314  
DEFINITION wx17b12.r1 Soares mouse NMU Mus musculus cDNA clone IMAGE:660447 5',  
similar to TX:G1136414 G1136414 KIAA0177 PROTEIN ;, mRNA sequence.  
ACCESSION AA237314  
VERSION AA237314.1 GI:1861335  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

## REFERENCE AUTHORS

Eukaryota; Eutelezoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus.  
1 (bases 1 to 97)  
Marrs, M., Hillier, L., Allen, M., Bowles, N., Dietrich, N., Dubucque, T., Geisel, S., Kucher, T., Lucy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE  
JOURNAL  
COMMENT

The WashU-HHMI Mouse EST Project  
Unpublished (1996)  
Contact: Maira W/Mouse EST Project  
WashU-HHMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
tel: 314 286 1800

## FEATURES

## Source

```

1. .97
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:680447"
/tissue_type="Liver"
/lab_host="DH10B"
/clone_lib="Soares mouse NML"
/note="Vector: pRT7D-Pac (Pharmacia) with a modified
polylinker. Site.1: Not I; Site.2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'.
TGTTACCAATCTGAAGCGGAGCGCGCGCACTTTTTTTTTTTT 3'] ;
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pRT73 vector. Library
constructed and normalized by Bento Soares and M.Fátima
Conaúdo."

```

**ORIGIN**

Very Match	42.14;	Score 16;	DB 1;	Length 97;
Subst Local Similarity	58.34;	Pred. No. 4.2e+04;		
Indels	5;	Mismatches	5;	Gaps 0;
Conservative	14;			

```

QY      6 AATCUGAUGAGGCGCCGUAGGCCGA 29
          | : : | | | | : : | | |
Db      69 ATTTGATGAGGACTTTAGCCCGA 92

```

RESULT	19
AZ391476/c	
LOCUS	AZ391476
DEFINITION	65 bp DNA linear GSS 03-OCT-2000 IM0153C11R Mouse 10kb plaemid UOEC1M library Mus musculus genomic clone UOEC1M0153C11 R, genomic survey sequence.

TITLE	JOURNAL
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	Unpublished (2000)

**COMMENT**

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0153 row: C column: 11  
Seq primer: CACACAGGAACAACGATATGACC  
Class: plasmid ends  
High quality sequence stop: 65.

**FEATURES**

**SOURCE**

1. .65  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGGCM0153C11"  
/sex="Male"  
/lab\_host="B. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb Plasmid UGGCM library"  
/note="Vector: PM04294; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resource/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PM042 (gi|4732114|gb|AF128072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent B. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN

Query Match	41.6%	Score 15.8;	DB 8;	Length 65;
Best Local Similarity	59.3%;	Pred. No. 4.9e+04;		
Matches 16; Conservative	4;	Mismatches 7;	Indels 0;	Gaps 0;

```
QY . 1 CCUGCAUCUGAUGAGGCCCGUAGGCC 27
      ||| : | : ||||| : |||||
Db 27 CCTTCTTCCAGTAGGCGATAGGCC 1
```

RESULT 20			
LOCUS	CA587380/c		
DEFINITION	IBEL1P67P cDNA from mouse aorta Mus musculus CDNA, mRNA sequence.	69 bp	linear
ACCESSION	CA587380		EST 12-JAN-2004

**REFERENCE**  
1 (bases 1 to 69)  
**AUTHORS**  
Bohrang S., Andersson T., Theilj A., Odberg J. and Lundberg J.  
**TITLE**  
Vascular gene expression in atherosclerotic plaque prone regions  
analysed by representational difference analysis  
**JOURNAL**  
Unpublished (2002)  
**COMMENT**  
Contact: Andersson Tove  
Department of Biotechnology  
KTH  
Tekniskringen 34, plan 6, 100 44 Stockholm, Sweden



**TITLE** Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification method

**JOURNAL MEDLINE** Genome Res. 11 (9), 1553-1558 (2001)

**PUBMED** 115429098

**COMMENT** 11544199

Contact: George J. Kargul

Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@igsun.grc.nia.nih.gov  
nlaest: cdna@igsun.grc.nia.nih.gov/cdna/cdna.html  
Plate: L0955 row: G column: 10  
Seq primer: -21M3 Reverse  
High quality sequence stop: 89  
POLYA=No.

# **FEATURES**

**source** Location/Qualifiers

1..89

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="nlaest:L0955G10-5"

/db\_xref="taxon:10090"

/clone="L0955G10"

/issue\_type="Newborn Kidney"

/dev\_stage="Newborn"

/lab\_host="D10B"

/clone\_1lb="NIA Mouse Newborn Kidney cDNA Library2 (short)"

/note="Vector: pSPORT1 (Invitrogen); Site.1: SalI; Site.2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cdna). This is a short-transcript enriched cDNA library (Ref. Genome Res. 11:1553-1558 (2001). [PMID: 11544199]). In brief, double-stranded cDNAs were synthesized with an Oligo(dt) primer (Invitrogen: 5'-PACACTGATCTGATCGCAGCGCCGCTTTT-3') from 26 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L0-salI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer SalI-L. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 1.5 kb. The library was constructed by Yulan Plao (NIA)."

## **ORIGIN**

**Query Match** 41.6%; Score 15.8; DB 4; Length 89;

**Best Local Similarity** 63.0%; Pred. No. 5.1e+04;

**Matches** 17; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

**QY** 11 GAUGAGGCGGUAAGCGGAAAUAUCAG 37

**Db** 67 GATGGGCTGTAGGCCAATGAATGAG 41

**RESULT 24** CG663893 92 bp mRNA linear GSS 02-OCT-2003

**LOCUS** CG663893

**DEFINITION** OST450022 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST450022, mRNA sequence.

**ACCESSION** CG663893

**VERSION** CG663893.1 GI:37487742

**KEYWORDS** GSS.

**SOURCE** Mus musculus (house mouse)

**ORGANISM** Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## **REFERENCE**

**AUTHORS** Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 92)

Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Piggett,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A., Fiddie,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jiang,C., Key,B.W., Jr., Kipp,P., Kohhauff,B., Ma,Z.-Q., Marresch,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Sigtlenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.

Wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

Contact: Zambrowicz BP

Omnibank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene trap.

## **FEATURES**

**source** Location/Qualifiers

1..92

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="129Sv/Ev"

/db\_xref="taxon:10090"

/clone="OST450022"

/cell\_type="embryonic stem cell"

/clone\_1lb="Mus musculus 129Sv/Ev"

## **ORIGIN**

**Query Match** 41.6%; Score 15.8; DB 9; Length 92;

**Best Local Similarity** 50.0%; Pred. No. 5.2e+04;

**Matches** 18; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

**QY** 1 CCUGAUCUGAUGAGCGCGUAGCGGAAAUAUCA 36

**Db** 44 CCTGCAACTCCTCAGCCCGTAGTCVNACAGTCA 9

**RESULT 25** CD947628 94 bp mRNA linear EST 15-JUL-2003

**LOCUS** SAA.70 GeneTag2 Zea mays cDNA, mRNA sequence.

**DEFINITION** CD947628

**ACCESSION** CD947628.1 GI:32795392

**KEYWORDS** EST.

**SOURCE** Zea mays

**ORGANISM** Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.

## **REFERENCE**

**AUTHORS** Genoplatte.

**TITLE** Genoplatte, a major partnership french program in plant genomics Unpublished (2003)

**JOURNAL** Contact: Genoplatte

**COMMENT** Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplatte' (http://www.genoplatte.com and http://genoplatte-info.infobiogen.fr).

## **FEATURES**

**source** Location/Qualifiers

1..94

/organism="Zea mays"

/mol\_type="mRNA"

/culturvar="mixture"

/db\_xref="taxon:4577"

/clone\_1lb="GeneTag2"

## **ORIGIN**

Query Match 41.6%; Score 15.8; DB 6; Length 94;  
 Best Local Similarity 66.7%; Pred. No. 5.2e+04;  
 Matches 18; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 7 AUGAGAGCGCGGCGGAAAAA 33  
 |||||  
 Db 67 ACCAGAGAGCGCCATTGAGGAAAAA 41

RESULT 26  
 CV519527 94 bp mRNA linear EST 06-OCT-2004  
 LOCUS 0089P00302.x0\_E02 Mimulus guttatus library 2 Mimulus guttatus cDNA  
 DEFINITION Clome 0089P00302.x0\_E02, mRNA sequence.  
 ACCESSION CV519527  
 VERSION CV519527  
 KEYWORDS GI:53846059  
 SOURCE EST.  
 ORGANISM Mimulus guttatus (spotted monkey flower)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamiales; Lamiales; Lamiaceae; Mimosaceae;  
 Mimulus.

REFERENCE 1 (bases 1 to 94)  
 WILLIS, J., VISION, T., DIETRICH, F.S. and ALLEN, A.  
 TITLE Mimulus guttatus cDNA sequence  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Willis J  
 Department of Biology  
 Duke University  
 072-A Biological Sciences Science Drive, Durham, NC 27708, USA  
 Tel: 919 660 7340  
 Fax: 919 660 7293  
 Email: jwillis@duke.edu  
 Plate: 0089P0030 row: 02 column: E  
 Seq primer: T7  
 High quality sequence stop: 667.  
 Location/Qualifiers  
 1..94  
 /organism="Mimulus guttatus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4155"  
 /clone="0089P00302.x0\_E02"  
 /clone\_lib="Mimulus guttatus library 2"  
 /note="Vector: pGEM-T Easy; a Mimulus guttatus cDNA library"

FEATURES  
 source  
 1..94  
 /organism="Mimulus guttatus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4155"  
 /clone="0089P00302.x0\_E02"  
 /clone\_lib="Mimulus guttatus library 2"  
 /note="Vector: pGEM-T Easy; a Mimulus guttatus cDNA library"

## ORIGIN

Query Match 41.6%; Score 15.8; DB 7; Length 94;  
 Best Local Similarity 66.7%; Pred. No. 5.2e+04;  
 Matches 18; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 12 AUGAGCGCGUAGCGCGAAAAAUCAG 38  
 |||||  
 Db 51 AAGTCTCTGCTAAGCGGAAAAATTCAG 25

RESULT 27  
 CG528153 94 bp mRNA linear GSS 01-OCT-2003  
 LOCUS OST107142 Mus musculus 1295v/Ex Mus musculus cDNA clone OST107142,  
 DEFINITION mRNA sequence.  
 ACCESSION CG528153  
 VERSION CG528153.1 GI:37314725  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 94)  
 Zambrowicz, B.P., Abujin, A., Ramirez-Solis, R., Richter, J.J.,  
 Pigott, J., Beltrandelito, H., Buxton, E.C., Edwards, J., Finch, R.A.,  
 Fridtjof, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaling, C.,

REFERENCE  
 AUTHORS

Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,  
 Payre, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,  
 Sparks, M.D., Van Slichtenhorst, I., Vogel, P., Walke, W., Xu, N.,  
 Zhu, Q., Person, C. and Sands, A.T.  
 Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
 screen to identify potential targets for therapeutic intervention  
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
 Contact: Zambrowicz BP  
 OmniBank  
 Lexicon Genetics Incorporated  
 4000 Research Forest Drive, The Woodlands, TX 77381, USA  
 Email: material@lexgen.com  
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
 Class: Gene Trap.  
 Location/Qualifiers  
 1..94  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129Sv/Ev"  
 /db\_xref="taxon:10090"  
 /clone="OST107142"  
 /cell\_type="embryonic stem cell"  
 /clone\_lib="Mus musculus 129Sv/Ex"

## FEATURES

source

Query Match 41.6%; Score 15.8; DB 9; Length 94;  
 Best Local Similarity 57.1%; Pred. No. 5.2e+04;  
 Matches 20; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

OY 3 UGCAUUCUGAGCGCGGCGGAAAAAUCAG 37  
 |||||  
 Db 17 TGAACCTGAGAGATGAGGCGGAAAAATTCAG 51

RESULT 28  
 A2608536 97 bp DNA linear GSS 13-DEC-2000  
 LOCUS 1M0432N13R Mouse 10kb plasmid UGCLM library Mus musculus genomic  
 DEFINITION clone UGCLM0432N13 R, genomic survey sequence.  
 ACCESSION A2608536  
 VERSION A2608536  
 KEYWORDS GI:11730726  
 SOURCE GSS.  
 ORGANISM Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 97)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausen, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0432 row: N column: 13  
 Seq primer: CACACGAGAACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 97.  
 Location/Qualifiers  
 1..97  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57Bl/6J"

## REFERENCE

AUTHORS

## TITLE

JOURNAL

COMMENT

## FEATURES

source

/db\_xref="taxon:10090"  
/clone="UUGC1M0432N13"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 41.6%; Score 15.8; DB 8; Length 97;  
Best Local Similarity 54.3%; Pred. No. 5.2e+04;  
Matches 19; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 4 GCATUCGAGAGCGCCGUAAGCCGAGAAAUACAG 38  
DB 92 GCATATGGCGAGATTAGACAGACTCAGG 58

RESULT 29  
AZ481971 98 bp DNA linear GSS 04-OCT-2000  
LOCUS AZ481971/c  
DEFINITION 1M030608R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M030608 R, genomic survey sequence.  
ACCESSION AZ481971 GI:10643036  
VERSION  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 98)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmud, M., Meenen, B., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Place: 0306 row: J column: 08  
Seq primer: CACACAGGAAACAGCATATGACC  
Class: plasmid ends  
High quality sequence scop: 98.  
Location/Qualifiers  
1..98  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"

## FEATURES

1..98  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"

/db\_xref="taxon:10090"  
/clone="UUGC1M0306J08"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 41.6%; Score 15.8; DB 8; Length 98;  
Best Local Similarity 73.7%; Pred. No. 5.2e+04;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 13 UGAGCCGUAAGCCGAGAA 31  
DB 75 TGAGCCCTTTAGCCTTAA 57

RESULT 30  
AZ566002 98 bp DNA linear GSS 07-MAY-2001  
LOCUS AZ566002  
DEFINITION 21SPB01 PV MBN #16 (amplified twice) Plasmodium vivax genomic 3',  
genomic survey sequence.  
ACCESSION AZ566002 GI:13972489  
VERSION  
KEYWORDS GSS.  
SOURCE Plasmodium vivax (malaria parasite P. vivax)  
ORGANISM Plasmodium vivax  
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
1 (bases 1 to 98)  
Carlton, J.M., R. and Dame, J.B.  
The Plasmodium vivax and P. berghei gene sequence tag projects  
Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)  
Contact: Dame JB  
Dept. of Pathobiology, College of Veterinary Medicine  
University of Florida  
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA  
Tel: 352 392 4700  
Fax: 352 392 9704  
Email: damej@mail.vetmed.ufl.edu  
Seq primer: M13(-20) forward  
Class: Shotgun.  
Location/Qualifiers  
1..98  
/organism="Plasmodium vivax"  
/mol\_type="genomic DNA"  
/strain="Belem"  
/db\_xref="taxon:5855"  
/dev\_stage="asexual blood forms"  
/lab\_host="Saimiri boliviensis"  
/clone\_lib="PV MBN #16 (amplified twice)"  
/note="Vector: Lambda zap II (Stratagene); individual  
clones excised into phagemid pBluescript; Site 1: EcoR I;  
Site 2: EcoR I; Genomic DNA was prepared from asynchronous  
blood stage forms of the Belem line of P. vivax grown in  
squirrel monkeys. Parasitized erythrocytes were purified

## FEATURES

1..98  
/organism="Plasmodium vivax"  
/mol\_type="genomic DNA"  
/strain="Belem"  
/db\_xref="taxon:5855"  
/dev\_stage="asexual blood forms"  
/lab\_host="Saimiri boliviensis"  
/clone\_lib="PV MBN #16 (amplified twice)"  
/note="Vector: Lambda zap II (Stratagene); individual  
clones excised into phagemid pBluescript; Site 1: EcoR I;  
Site 2: EcoR I; Genomic DNA was prepared from asynchronous  
blood stage forms of the Belem line of P. vivax grown in  
squirrel monkeys. Parasitized erythrocytes were purified

from contaminating host leukocytes by filtration of ADP activated blood through acid-washed glass beads and Whatman CFl cellulose columns by gravity filtration. Purified DNA was digested with mung bean nuclease in the presence of 42.5% formamide at 500C as described (Gallinski, M. et al. 1992. Cell 69,1213-1226; Vernick, K.D. et al.1988. N.A.R. 16, 6883-6896). Eco RI linkers were added and the constructs ligated into Lambda ZAP II. P. vivax Belem was originally isolated from a patient in Belem, Brazil 1980 by Mercia de Arruda, adapted to Saimiri monkeys by Jurg Gysin, and maintained since 1983 in squirrel monkeys."

## ORIGIN

Query Match 41.6%; Score 15.8; DB 8; Length 98;

Best Local Similarity 54.3%; Pred. No. 5.2e+04;

Matches 19; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 2 CUGCAUUCUGAUGAGCCGCUUAGCCGAAAUCA 36  
18 CTGCAAAAGGCTTATTCAGTTAGGAAGAAAGCA 52

LOCUS AJ590916 41 bp DNA linear GSS 15-JAN-2004  
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 576H02, genomic survey sequence.

ACCESSION AJ590916 GI:37940540  
VERSION GSS; left border; T-DNA flanking sequence.  
KEYWORDS Arabidopsis thaliana (thale cress)  
SOURCE Arabidopsis thaliana

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL MEDLINE 22363535  
PUBMED 12446565

REFERENCE 2 (bases 1 to 41)  
Balzerque, S.

AUTHORS Direct Submission  
TITLE Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'genoplante' (<http://www.genoplante.com> and <http://genoplante-info.inbioigen.fr>).

## FEATURES

source

1..41 Location/Qualifiers

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/culivar="Wassiljewskij3a"

/db\_xref="taxon:3702"

/clone="576H02"

/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"

/note="T-DNA flanking sequence left border"

Query Match 41.1%; Score 15.6; DB 9; Length 41;  
Best Local Similarity 52.6%; Pred. No. 5.6e+04;  
Matches 20; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 CCUGCAUUCUGAUGAGCCGCUUAGCCGAAAUCAAGC 38  
2 CCAAAAGCTGACGAAGACGTTACGACGAGAGAGAGG 39

RESULT 32  
AT702572 76 bp mRNA linear EST 18-DEC-1999

LOCUS we80b03.x1 Soares NPL T GBC S1 Homo sapiens cDNA clone IMAGE:2347373 3', mRNA sequence.

ACCESSION AT702572  
VERSION AT702572.1 GI:4990472

KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 76)  
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

UNPUBLISHED (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)

This clone is available royalty-free through LNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Insert Length: 544 Std Error: 0.00  
Seq primer: -40UP from Gldco

High quality sequence stop: 65.

## FEATURES

source

1..76 Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2347373"

/lab\_host="BDH10B"

/clone\_lib="Soares\_NPL\_T\_GBC\_S1"

/note="Organ: pooled; Vector: pTT73D-Pac (Pharmacia) with a modified polylinker; Site: 1: Not I; Site 2: Eco RI;

Equal amounts of plasmid DNA from three normalized libraries (fetal lung MBH19W, testis NBT, and B-cell NCI CGAP GCB) were mixed and ss circles were made in vitro. Following HAP purification, this DNA was used as

tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of

1.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento

Soares and M. Patricia Bonaldi.

## ORIGIN

Query Match 41.1%; Score 15.6; DB 1; Length 76;  
Best Local Similarity 68.2%; Pred. No. 6.1e+04;

Matches 15; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 11 GAUGAGCGCGUAGCCGCGAANA 32  
13 GATGGGCTTTAGGCGCGAANA 34

## RESULT 33

LOCUS W72704

DEFINITION zd71c05.61 Soares fetal heart MbH19W Homo sapiens cDNA clone IMAGE:346088 3' similar to PIR:A26882 A26882 PIR2 hypothetical protein - rat; mRNA sequence.

76 bp mRNA linear EST 17-OCT-1996  
protein - rat; mRNA sequence.

ACCESSION W72704  
VERSION W72704.1 GI:1382701

ORIGIN

KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Buiakytca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 76)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
TITLE The Maestri-Merc EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Insert Length: 1248 Std Error: 0.00  
Seq primer: mob.REGA+ET  
High quality sequence stop: 1.  
Location/Qualifiers  
1..76  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:1271463"  
/db\_xref="taxon:9606"  
/clone\_image="346088"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal heart NBHL19W"  
/note="Organ: heart; Vector: pT73D (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TCTTACCAATCTGAGATGGAGCGCCGATCTTTTCTTTTCTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by  
M.Facima Bonaldo. This library was constructed from the  
same fetuses as the fetal lung library, Soares fetal lung  
NBHL19W."

ORIGIN  
Query Match 41.1%; Score 15.6; DB 7; Length 76;  
Best Local Similarity 52.6%; Pred. No. 6.1e+04;  
Matches 20; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 1 CCUGCAUUCGAGGCGCGUAGCGCGAAGAAUACAG 38  
23 CTTCAATCAAGAGCTCCGCTGAGCTTGAATGAGG 60

Db

RESULT 34  
CG547582/c 78 bp mRNA linear GSS 01-OCT-2003  
LOCUS OST148394 Mus musculus 129SV/Ev Mus musculus cDNA clone OST148394,  
DEFINITION mRNA sequence.  
ACCESSION CG547582  
VERSION CG547582.1 GI:37334169  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Buiakytca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 78)

AUTHORS Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,  
Piggott, J., Beltrande-Rio, H., Buxton, E.C., Edwards, J., Finch, R.A.,  
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jang, C.,  
Key, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,  
Payne, R., Porter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,  
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,  
Zhu, Q., Person, C., and Sands, A.T.  
TITLE Wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
COMMENT Contact: Zambrowicz BP  
OmitBank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: material@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)  
Class: Gene Trap.  
Location/Qualifiers  
1..78  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129SV/Ev"  
/db\_xref="taxon:10090"  
/clone\_image="OST148394"  
/cell\_type="embryonic stem cell"  
/clone\_lib="Mus musculus 129SV/Ev"

ORIGIN  
Query Match 41.1%; Score 15.6; DB 9; Length 78;  
Best Local Similarity 50.0%; Pred. No. 6.2e+04;  
Matches 19; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 CCUGCAUUCGAGGCGCGUAGCGCGAAGAAUACAG 38  
39 CCGTCTCTGGAGGAGATCTGAAGCGCACTTAGG 2

Db

RESULT 35  
CG545569 80 bp mRNA linear GSS 01-OCT-2003  
LOCUS OST143941 Mus musculus 129SV/Ev Mus musculus cDNA clone OST143941,  
DEFINITION mRNA sequence.  
ACCESSION CG545569  
VERSION CG545569.1 GI:37332156  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Buiakytca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 80)

AUTHORS Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,  
Piggott, J., Beltrande-Rio, H., Buxton, E.C., Edwards, J., Finch, R.A.,  
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jang, C.,  
Key, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,  
Payne, R., Porter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,  
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,  
Zhu, Q., Person, C., and Sands, A.T.  
TITLE Wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
COMMENT Contact: Zambrowicz BP  
OmitBank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: material@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)  
Class: Gene Trap.  
Location/Qualifiers  
1..80  
/organism="Mus musculus"  
/mol\_type="mRNA"



VERSION BG881971.1 GI:14259063  
 KEYWORDS EST.  
 SOURCE Glycine max (soybean)  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustersids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 1 (bases 1 to 99)  
 Shoemaker R., Kelm, P., Vodkin, L., Erpelting, J., Corryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Peterson, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
 Public Soybean EST Project  
 Unpublished (1999)  
 Contact: Shoemaker R./Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.wustl.edu  
 When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)  
 Insert Length: 1306 Std Error: 0.00  
 High quality sequence stop: 99.  
 Location/Qualifiers  
 1..99  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /cultivar="Williams"  
 /db\_xref="taxon:3847"  
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl065-3196"  
 /tissue\_type="germinating shoots"  
 /lab\_host="DH10B"  
 /clone\_1ib="Gm-cl065"  
 /note="Vector: Bluescript II SK+, Site 1: EcoRI, Site 2: XhoI; The cDNA library was constructed from mRNA isolated from germinating shoots of the cultivar Williams. The seeds were allowed to germinate for 24 hours prior to being cold stressed for 2 days at 4C. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the Bluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN  
 Query Match 41.1%; Score 15.6; DB 4; Length 99;  
 Best Local Similarity 52.6%; Pred. No. 6.4e+04;  
 Matches 20; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 1 CCUGCAUUGAGAGCGCGUAGCGCGAANAUCAGG 38  
 Db 51 CTTCAATCTGGTGGAGCCCTCAAGGCTACAGATG 14

RESULT 39  
 CV316867 100 bp mRNA linear EST 24-SEP-2004  
 LOCUS CM2-BN0185-220400-166-h02 BN0185 Homo sapiens cDNA, mRNA sequence.  
 DEFINITION CV316867  
 ACCESSION CV316867  
 VERSION CV316867.1 GI:52640081  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
 1 (bases 1 to 100)  
 Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 MEDLINE 10737800  
 PUBMED  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. <http://www.ludwig.org.br>.  
 Location/Qualifiers  
 1..100  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_1ib="BN0185"  
 /note="Organ: breast normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORFESTS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN  
 Query Match 41.1%; Score 15.6; DB 7; Length 100;  
 Best Local Similarity 53.3%; Pred. No. 6.4e+04;  
 Matches 16; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 9 CUGAUGAGCGCGUAGCGCGAANAUCAGG 38  
 Db 52 CTTTGAGGCGGTCTGGGATCGATCTGG 23

RESULT 40  
 CC483070 51 bp DNA linear GSS 16-JUN-2003  
 LOCUS CH240\_311L11.TARAC13P2 CHORI-240 Bos taurus genomic clone  
 DEFINITION CH240\_311L11, genomic survey sequence.  
 ACCESSION CC483070  
 VERSION CC483070.1 GI:31764069  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 51)  
 Holt, R., Scott, J., Yang, G., Barber, S., Smaliv, D., Prabh, A.-L., Tsai, M., Cloutier, A., Lee, D., Girm, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., de Jong, P., McWilliam, S., Baris, W., Dalrymple, B.P. and Tellam, R.  
 Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398  
 Unpublished (2003)  
 Other\_GSSs: CH240\_311L11.T7

TITLE  
 JOURNAL  
 COMMENT

Contact: Rob Holt

Sequencing

The British Columbia Cancer Agency Genome Science Centre  
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4B6

Tel: 604-877-6085

Fax: 604-877-6276

Email: rholt@bccgsc.ca

Clones are derived from the bovine BAC library CHORI-240

(<http://www.chori.org/bacpac/bovine240.htm>). For BAC library availability, please contact Pieter de Jong ([pdejong@mail.cho.cho.org](mailto:pdejong@mail.cho.cho.org)).

Clones may be purchased from BACPAC Resources

(<http://www.chori.org/bacpac/ordering/information.htm>). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.

Plate: 311 row: L column: 11

Seq primer: SP6

Class: BAC ends.

#### FEATURES

source

1. .51 Location/Qualifiers

/organism="Bos taurus"

/mol\_type="genomic DNA"

/strain="breed: Hereford"

/db\_xref="taxon:9913"

/clone="CH240\_311L11"

/sex="Male"

/cell\_type="Blood"

/clone\_lib="CHORI-240"

/note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

#### ORIGIN

Query Match

40.5%; Score 15.4; DB 9; Length 51;

Best Local Similarity 60.0%; Pred. No. 7.1e+04;

Matches 15; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 5 CAUCUGANGAGCCGCUUNGCCGA 29

Db 26 CGACCTGATGAGTCGTGGACAA 50

Search completed: May 13, 2005, 17:51:09  
Job time : 1864.87 secs